

# STIC Search Report Biotech-Chem Library

## STIC Database Tracking Number: 144864

TO: Jeffrey Parkin

Location: rem/3d39/3c18

Art Unit: 1648

Monday, February 28, 2005

Case Serial Number: 09/319156

From: Deirdre Arnold

**Location: Biotech-Chem Library** 

**REM 1A64** 

Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

### Search Notes

Please contact me if you encounter any problems with the disk or files.

Note that results are not generally sent via e-mail because the files are often very large.

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards, Deirdre Arnold



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#### STIC-Biotech/ChemLib

1448ldf

From:

Parkin, Jeffrey

Sent:

Wednesday, February 09, 2005 9:52 PM

To: Subject: STIC-Biotech/ChemLib U.S. Serial No. 09/319,156

Please search SEQ ID NOS.: 6, 9, and 12 from the aforementioned application v. all relevant databases, including interference.

Place results on both PAPER and electronic format (i.e., e-mail).

Provide the first 40 results for each search.

Thanks!

JSP AU 1648 REM 3D39 2-0908

<a href="http://expoweb1:8001/cgi-bin/expo/GenInfo/snquery.pl?APPL\_ID=09319156">http://expoweb1:8001/cgi-bin/expo/GenInfo/snquery.pl?APPL\_ID=09319156</a>

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Online Time:\_

Searcher: Anold
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Date Searcher Picked up: Date Completed: Searcher Prep/Rev. Time:

Type of Search
NA Sequence: #\_\_\_\_\_\_
AA Sequence :#\_\_\_\_\_\_
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Bibliographic:
Litigation:
Patent Family:
Other:

Vendors and cost where applicable

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WWW/Internet:\_\_\_\_
Other(Specify):\_\_\_\_\_\_

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Human chr Homo sapi

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AL07153 H
AP002790 H
AC064801 H
AL121784 H
AL135818 H
AC109992 H
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Retroyiral nucleic material and nucleotide fragments, in particular, associated with multiple sclerosis and/or rheumatoid arthritis, for diagnostic, prophylactic and therapeutic uses Patent: JP 2002509437-A 5 26-MAR-2002;
S. Unidentified
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7-JUL-1998 JP 1999508255
07-JUL-1997 FR 97/08816
GLAUCIA PARAHNOS BACCALA, FIORENCE KOMURIAN PRADEL, FREDERIC
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Strandedness: Single;
Topology: Linear;
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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PAT 18-SEP-2002

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RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR
ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR
DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES
BATCHI: WO 9902666-A 6 21-JAN-1999;
BIO MERIEUX (FR); OTT CATHERINE (FR)
LOCATION/QUALIFIER
                                                                                                                                                                                                                                        CTGGACCGGCCTGCTAGCCCCATGCTCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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1 (bases 1 to 635)

1 (bases 1 to 635)

Perron, H., Beseme, F., Bedin, F., Paranhos-Baccala, G.,
Komurian-Pradel, F., Jolivet-Reynaud, C. and Mandrand, B.

Isolated nucleotide sequences associated with multiple rheumatcoid arthritis and a process of detecting

Patent: US 6582703-A 102 24-UNN-2003;

Location/Qualifiers
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Sequence 102 from patent US 6582703.
AR344385.1 GI:33740326
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                /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Best Local Similarity
Matches 635; Conserv
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PAT 10-MAR-2000

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Multiple sclerosis associated retrovirus element
Viruses, Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses;
I (bases 1 to 2004)
S Komurian-Pradel, F., Paranhos-Baccala, G., Bedin, F.,
Ounanian-Pradel, F., Sodoyer, M., Ott, C., Rajoharison, A., Garcia, E.,
Mallet, F., Mandrand, B. and Perron, H.
Molecular cloning and characterization of MSRV-related sequences
associated with retrovirus-like particles
L Virology 260 (1), 1-9 (1999)
D 10405350
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Pred. No. 1.1e-189;
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167694 bp DNA linear PRI 25-APR-2002
Homo sapiens chromosome 18, clone RP11-622J9, complete sequence...
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AC113137.2 GI:19683504
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1910 CAACCCCCTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTCT 1969
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                                             Garcia, E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1370 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1730 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAATIGITCITCAAAIGGAGCACCAGAIGGAGTCCAIGACIAAGAICCACGIGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGGCTTGAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1670 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGATGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAGCACAGGGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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                                                                                                                                                                                                  retrovirus
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2 (bases 1 to 2004)
Komurian-Pradel,F., Paranhos-Baccala,G., Bedin,F.,
Ounanian-Paraz,A., Sodoyer,M., Ott,C., Rajoharison,A., (Mallet,F., Mandrand,B. and Perron,H.
Direct Submission
Submitted (10-FBB-1999) UMR103 CNRS, bioMerieux, 46, allorialie, Lyon 69007, France
                                                                                                                                                                                                                                                                                                                                                                                           Length 2004;
                                                                                                                                                                                                                                                                                                                                 region"
                                                                                                                                                                                         /organism="Multiple sclerosis associated element"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                          1. .2004
/note="gimilar to pol-env and 3'LTR
                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 635; DB 14;
100.0%; Pred. No. 1.3e-189;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTABATCTTGCAACTGABABABABABABABA 635
                                                                                                                                                                                                                                           /mol_type="mRNA"
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McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Muenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retterson, K., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retter, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Steaman, S., Swerery, P., Spencer, B., Stange-Thomann, N., Schainovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, N., Trajilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

All sequence, 320 Charles Street, Cambridge, MA 02141, USA On Mar 22, 2002 this sequence version replaced gi:1887526.

All repeats were identified using RepeatMasker: html

Lender: Whitchead Institute/ MIT Center for Genome Research Center: Whitchead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-11 Human Male BAC"
2566. .2593
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complement (12442. .13393)
/rpt_family="L1PA16"
13550. .13907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (8120. .8302)
/rpt family="LiM4"
complement (8444. .8971)
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complement (8973. .9386)
/rpt family="LiME3A"
complement (9387. .9690)
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9898. .10407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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6723. 6750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="AT_rich"
6982. .7280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2566. 72593
/rpt_family="AT_rich"
31087. 3127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone name: 622_J_9
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/rpt family="(TA)n"
3128. .3153
/rpt family="(TG)n"
3154. .3208
/rpt family="(TA)n"
complement (3212. .381)
/rpt family="rlMA9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt family="L1MB3"
5234. .6028
/rpt family="L1MB3"
complement (6259. .647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt family="MLT1E3"
1218. .115cc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="Aluy"
780. .7811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="RP11-622J9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
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Significant, B., Mitton, L., Nusbaum, C., Lander, E., Ali, M., Allen, N., Anderson, S., Barran, N., Bastlere, V., Bogulajarky, L., Boukhagaller, B., Anderson, S., Barran, N., Bastlere, V., Bogulajarky, L., Boukhagaller, B., Anderson, S., Barran, N., Bastlere, V., Gangolajarky, M., Colamon, P., Colamon, P., Canapolano, A., Chang, J., Chasaro, B., Choopel, Y., Colamon, M., Canapolano, A., Chang, J., Choopel, S., Gord, S., Goyette, M., Grahm, L., Ordan, P., Erro, S., Ferris, S., Cock, S., Goyette, M., Grahm, L., Ordan, P., Erro, S., Ferris, S., Lander, B., Marchalano, K., Mallar, M., Mand, M., Mallar, R., Mallar, M., Mallar, R., Mallar, M., Mallar, M., Mallar, R., Mallar, M., Mallar, M.,
                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I bases I to 167594)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo. sapiens chromosome 18; clone RP11-62209
                                                                                                                                                                                                                                                 (bases 1 to 167694)
                                                                                                                                                                                                                        Jnpublished
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JOURNAL
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AUTHORS
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AUTHORS
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JOURNAL
REFERENCE
AUTHORS
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AUTHORS
                                         KEYWORDS
SOURCE
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us-09-319-156b-6.rge

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2E C (bases 1 to 176095)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Choepel, Y., Colangelo, M., Borwi, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Domino, M., Doyle, M., Fenestor, J., Cerreira, P., Fitzhugh, M., Porrest, C., Gadse, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Liau, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McErnan, K., Machon, T., O'Donnell, P., Molurk, A., Maylor, J., Norman, C.H., O'Connor T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (02-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 25, 2001 Lhis sequence version replaced gi:7230183.

All repeats were identified using RepeatMasker:
Smit, A. F. A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                    123369 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 123310
                                                                                                                                         123190
                                                                                                                                                                                                             123130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC019346 176095 bp DNA linear HTG 25-OCT-2001
Homo sapiens chromosome 18 clone RP11-497M7 map 18, WORKING DRAFT
SEQUENCE.
                                                                                                                                                                            480
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Catarrhini, Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                           ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                                                                                                                                                  481 AGAGCACAGGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                        GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGACCAATCAGAGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 18, clone RP11-497M7 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                123009 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAAA 122975
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ACC19346.4 GI:16418201
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
HOMO sapiens (human)
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Mammalia; Eutheria; Primates;
1 (bases 1 to 176095)
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KEYWORDS
SOURCE
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AC019346/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
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Pred. No. 2.9e-188;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                             .. 2488ē. .24913

/rpt family="AT_rich"

25154. .25156

/note="single clone coverage"

25189. .25193

/note="<30 qual SNGL region"

complement (26144. .26248)

/rpt family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family="MLT1H"
                                                                                                                                                                                                                                                                                                rpt family="L1MB3"
omplement(20633. .22006)
rpt family="L1P"
2008. .22831
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complement(32304. .34133)
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rpt_family="AT_rich"
4886. .24913
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rpt family="(TAGA)n"
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                                                                                                                                                                                           ,,oo4. .18430
/rpt_family="L1PA4"
18441. .1900
                                                                                                                                                                                                                                                                                                                                                                /rpt_family="L1MB3"
22853. 23516
/rpt_family="L2"
24420. 24468
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family="MER67C"
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                                                                                                                                                 rpt family="(TA)n"
8013. .28078
                                  'rpt_family="L1PB1"
5633. .15912
                                                                              rpt_family="(TA)n"
5920. .16279
                                                                                                                                                                                                                                                                                            family="L1MB3"
                                                                                                                 family="L1PB1"
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9293. .20623
                                                                                             .16279
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Best Local Similarity 99.79
Matches 633, Conservative
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191<u>2</u>.
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150044 AGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG 149985
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         540
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1 (bases 1 to 210336)
Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Mano, J., Komp, C., Kottler, S., Lam, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.M., Webb, C., Wilhelmy, J., Yu, S. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-JAN-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Stanford DNA Sequencing and Technology Development
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      AGAGCACAGGGGAGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (Dases 1 to 210336)
Bruno,D., Conn,L., Dela Rosa,M., Federspiel,N., Foreman,P.,
Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
Yu,S. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing Vector: plasmid; plasmid_accession; 3% of read Sequencing Vector: plasmid; plasmid_accession; 3% of read Chemistry: Dye-primer; 10% of reads
Chemistry: Dye-terminator Big Dye; 88% of reads
Chemistry: Dye-terminator Big Dye; 88% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 208312 bases at least Q40
Consensus quality: 208317 bases at least Q30
Consensus quality: 208157 bases at least Q30
Insert size: 199765; agarose-fp
Insert size: 199765; agarose-fp
Quality coverage: 8.7x in Q20 bases; sum-of-contigs.
* NOTE: This is a "working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
------- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                     ACU22171

Homo sapiens chromosome 18 clone RP11-407C18, WORKING DRAFT SOCIENCE, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Mar 10, 2001 this sequence version replaced gi:13122770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC022171.18 GI:13270574
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN
Homo sapiens (human)
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Center clone name: RP11-407C18
------ Summary Statistics
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AUTHORS
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KEYWORDS
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Center project Information
Center project name: L4296
Center clone name: Sequencing vector: M3; M77815; 32% of reads
Sequencing vector: M3; M77815; 32% of reads
Sequencing vector: Plasmid; n/a; 68% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 176095 bases at least Q40
Consensus quality: 176095 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 176000; agarose-fp
Insert size: 176005; sum-of-contigs
Quality coverage: 11.5 in Q20 bases; agarose-fp
Quality coverage: 11.7 in Q20.
* NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
of the gaps between them are based on estimates that have
provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

I 176095; contig of 176095 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP11-497M7"
/clone_lib="RPCI-11 Human Male BAC"
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/db_xref="taxon:9606"
/chromosome="18"
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Matches
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Submitted (2-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAX 30, 2000 this sequence version replaced gi:6087973. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                      Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 148724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as trus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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2562: gap of 100 bp
7948: contig of 5386 bp in length
8048: gap of 100 bp
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                                                                                                       Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-2N15
Unpublished
             HTG; HTGS PHASE1; HTGS_DRAFT
Homo sapiens (human)
GI:7341824
                                                                                                                                                            (bases 1 to 148724)
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15900:
25059:
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41906:
                                               Homo sapiens
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           KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGACTGAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58476 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGCACAGGGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                              1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGGACCAATCAGAGAGCTC
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                            Length 210336;
                                                                                                                                                                                                                                                                                                                               ;
0
9 66568: gap of unknown length
9 210336: contig of 143768 bp in length.
Location/Qualifiers
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                                                                                                                                                  clone_lib="RPCI human BAC library 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAA 58810
                                                                                                                                                                                                                                                                                               Score 631.8; DB 2;
Pred. No. 3e-188;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAAAA 635
                                                                                                                                                            1. .66468
/note="assembly_name:Contig44
                                                                                                                                                                                                                                /note="assembly_name:Contig45
clone_end:SP6"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="RP11-407C18"
                                                                                                                                                                                                clone_end:T7"
66569. .210336
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.7%;
Matches 633; Conservative
     66469
66569
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AC010778/c
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contig of 21335 bp in length gap of 100 bp contig of 35146 bp in length

63341: 98587:

AC010778 148724 bp DNA linear HTG 30-MAR-2000 Homo sapiens clone RP11-2N15, WORKING DRAFT SEQUENCE, 8 unordered

pieces. AC010778

DEFINITION ACCESSION

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Direct Submission

Submitted (22-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

buring sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences

rhe following abbreviations are used to associate primary accession

numbers given in the feature table with their source databases:

EMS.; SWISSERCH; Tr.; TREMBL; Wp.; WORNPEP; Information

on the WORNPEP database can be found at

http://www.sanger.ac.uk/Projectsf1 clone contigs of human

chromosome X, constructed by the Sanger Centre Chromosome X Mapping

Group. Further information can be found at

http://www.sanger.ac.uk/HGP/ChrX

This sequence was finished as follows unless otherwise noted: all

regions were either double-etranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. RF6-19804 is from the

library RPCI-c constructed by the group of Pieter de Jong. For

further details see

http://www.chori.org/bacpac/home.htm

VECTOR: PRPAC.
                                                                                                                                           AL162912 8339 bp DNA linear PRI 22-NOV-2001
Human DNA sequence from clone RP6-198C4 on chromosome Xq13.3-21.2,
complete sequence.
                                                                                                                                                                                                                                                                                                                                     Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5635. .5673
/note="HERV17 repeat: matches 7419. .7457 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5930 of consensus"
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/note="LTR17 repeat: matches 1. .239 of consensus"
0595. :6280
/note="LTR17 repeat: matches 239. .324 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMPORTANT: This sequence is not the entire insert of clone RP6-198C4 It may be shorter because we sequence overlapping sections only once, except for a short overlap. Location/Qualifiers
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hote="HERV17 repeat: matches 8244. .8523 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . .56<u>4</u>1
note="HERV17 repeat: matches 368.
                     1. .8339
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="RPCI-6"
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/map="q13.3-21.2"
/clone="RP6-198C4"
                                                                                                                                                                                                                           AL162912 AL121824
AL162912.1 GI:7406722
                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 8339)
                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40271 CCCHGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATTGAAACTGTAAAACTA 40212
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  8 98687: gap of 100 bp
8 148724: contig of 50037 bp in length.
Location/Qualifiers
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                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
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/clone="RR11-2N15"
/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 91.4%; Score 580.2; DB 2; Best Local Similarity 94.8%; Pred. No. 6.6e-172; Matches 600; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
2563. 7948
/note="assembly_fragment"
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note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                         vector side:right"
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Direct Submission
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
E. (bases 1 to 1360µ).
E. Hillier L.W.; Pulton,R.S.; Fulton,L.A.; Graves,T.A.; Pepin,K.H.;
Magner-McPherson,C., Layman,D.; Maas,J.; Jaeger,S.; Walker,R.;
Wylle,K.; Sekhon,M.; Becker,M.C.; O'Laughlin,M.D.; Schaller,M.E.;
Fewlel,G.A.; Delehaunty,K.D.; Miner,T.L.; Nash,W.E.; Cordes,M.;
Fewlel,G.A.; Vanbrunt,A., Nguyen,C.; D.; Mare,B.; Courtney,L.;
Kalicki,J.; Ozersky,P.; Belicki,L., Scott,K.; Holmes,A.;
Harkins,R.; Harris,A.; Strong,C.M.; Hou,S.; Tomlinson,C.;
Dauphin-Kohlberg,S.; Kozlowicz-Reilly,A.; Leonard,S.; Rohlfing,T.;
Strowmatt,C.; Latrellle,P.; Miller,N.; Johnson,D.; Murray,J.;
Strowmatt,C.; Latrellle,P.; Miller,N.; Johnson,D.; Murray,J.;
Woessner,J.P.; Wendl,M.C.; Yang,S.P.; Schultz,B.R.; Wallis,J.W.;
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                                                                                                    CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATTGAAACTGTAAAACTA 5723
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                                                                                                                                                                                                                                                     CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
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                                                                                                                                                     CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                                                                                                                                                                                                                                                                            181 GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
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                                                                            CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
                                        Gaps
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complete sequence.
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Length 8339;
                                      Indels
Score 579.2; DB 9;
Pred. No. 8.4e-172;
0; Mismatches 33;
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Homo sapiens BAC clone RP11-95P9 from 7,
AC073626
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Query Match
Best Local Similarity 94.8%;
Matches 599; Conservative
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Homo sapiens
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ACCESSION
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KEYWORDS
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Spieth, J., Bieri, T.A., Nelson, J.O., Berkowicz, N., Wohldmann, P.E., Cook, L.L., Hickenbotham, M.T., Eldred, J., Williams, D., Bedell, J.A., Marta, M.B.R., Clifton, S.W., Chissoe, S.L., Marra, M.A., Raymond, C., Haugen, E., Gillett, W., Zhou, Y., James, R., Phelps, K., Iadanoto, S., Bubb, K., Simms, E., Levy, R., Clendenning, J., Kaul, R., Kent, W.J., Furey, T.S., Baertsch, R.A., Brent, M.R., Keibler, E., Flicek, P., Chinwalla, M., Bailey, J.A., Portnoy, M.E., Torrents, D., Chinwalla, A.T., Gish, W.R., Eddy, S.R., McPherson, J.D., Olson, M.V., Eichler, E.E., Green, E.D., Waterston, R.H. and Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (27-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. 1
MO 63108, USA
Materston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing Center, Washington 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (30-JAN-2004) Department of Genetics, Washington Submitted (30-JAN-2004) Department of Genetics, Missouri 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University, 4444 Forest Park Avenue, St. Louis, Missouri 63
On Feb 16, 2001 this sequence version replaced gi:11597125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence of Homo sapiens BAC clone RP11-95P9 Unpublished (2001)
3 (bases 1 to 136901)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Genetics,
Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 136901)
Bauer, H., Haakenson, B. and Nguyen, C.
                                                                                                                                                                                                                                                                                                              Nature 424 (6945), 157-164 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-FEB-2001) Genome University School of Medicine, MO 63108, USA
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University, 4444 Forest
6 (bases 1 to 136901)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-APR-2003)
University, 4444 Forest
7 (bases 1 to 136901)
Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WUGSC
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Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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Web site: http://genome.wustl.edu Contact: sapiens@watson.wustl.edu Center project name: H\_NH0095P09 Summary Statistics

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

and The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information MAPPING INFORMATION:

us-09-319-156b-6.rge

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CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGA
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                                                                                                                                                                    16885..17023

- Typt family="MER1_type"

17189..17380

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/ rpt family="MER1_type"

/ rpt family="MRR"

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                                                                                          15997, .1643
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21716. 21879
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22121. 22550
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22576. 23085
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15457. .15494
/rpt_family="AT_rich"
| 15515. .1552
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15997. .16043
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23097. .24931
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/rpt_family="MIR"
18604 ...19120
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Best Local Similarity 93.7
Matches 595; Conservative
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                                                                                                                                                                                                                                 The clone sequenced to the left is CTD-2023N18, 200 bp overlap the clone sequenced to the right is CTA-250D13, 200 bp overlap. Actual start of this clone is at base position 127066 of CTD-2023N18 actual end is at base position 26937 of CTA-250D13.

Location/Qualifiers
                                                                   SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8 The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
      about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu
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7829...7823

7829...7823

7829...7985

7704...8064

8064...8064

8067...8206

7704...8206

7704...8206

7704...8206

7704...8206

7704...8208

7704...8288

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7704...8288

7704...8288

7704...8288

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7704...8388

7704...83884

7704...8384

7704...8384

7704...8384
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                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="7"
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/rpt. family="(TAA)n"

14453 . .14659

/rpt. family="MIR"

15191 . .15248
                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="RPCI-11"
545. 1149
'rpt family="L1"
1195. .1380
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1533. .1790
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2972. .3112
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4398. .14434
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rpt family="Alu"
0815. .10909
                                                                                                                                                                                                                                                                                                                                                                                                            clone="RP11-95P9"
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95558

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Score 571, DB 9; Length 136901; Pred. No. 5.4e-169; 0; Mismatches 40; Indels 0;

89.9%;

95498

180

95438

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95378

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Submitted (129-SEP-2011) Sanger Centre, Hinxton, Cambridgeshire, CBLO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 2, 2001 this sequence version replaced gi:14702155.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by a covered by as compressions are used to associate primary accession numbers given in the feature table with their source databases: EMBL; Sw:, SWISSRROT; Tr:, TREMBL; WORMPEP; Information on the WORMPEP here. A pression of the following and repeats all regions were series. EMBL; Sw:, SWISSRROT; Tr:, TREMBL; WORMPEP; Information on the WORMPEP here. A pression of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.chori.org/bacpac/home.htm
VECTOR: pBACG3.6
IMPORTANT: This sequence is not the entire insert of clone
SEP11-134K1 It may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true right end of clone RP11-134K1 is at 89728 in this
sequence. The true right end of clone RP11-60C15 is at 2000 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL583805
Human DNA sequence from clone RPI1-134K1 on chromosome 9, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 89728)
                           57476 ACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTTTTGCCTG
                                                                                                                                                                                                      481 AGAGCACAGCGGAAGAGACAAGGATGGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                         actarartigetartirgecararartregaggtrargarartregecartertitetig
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      GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
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AL583805 AC051658
AL583805.7 GI:15865009
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Direct Submission
Submitted (11-MAY-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
3 (bases 1 to 176188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (29-AUG-2002) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
On Aug 29, 2002 this sequence version replaced gi:14625082.
Location/Qualifiers
1. 176188
                                                                                                                                                                                                                 ACO68898 176188 bp DNA linear PRI 29-AUG-2002
Homo sapiens chromosome 10 clone RP11-534L6, complete sequence.
ACO68898
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176188)
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Pred. No. 1.6e-167;
0; Mismatches 41;
                                                                                  ATTAAATCTTGCAACTGAAAAAAAAAAAAAAA
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/db_xref="taxon:9606"
/chromosome="lo"
/clone="RR11-53416"
/clone_lib="RPCI-11"
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Local Similarity 93.5%;
Nes 591; Conservative 0
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Direct Submission
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Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 112405)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                               88.9%; Score 564.6; DB 9;
llarity 94.2%; Pred. No. 5.4e-167;
Conservative 0; Mismatches 34;
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                                                                         /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-134K1"
/clone_lib="RPCI-11.1"
                                                        sapiens,
location/Qualifiers
                         l. .89728
′organism="Homo
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Homo sapiens
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Alabrooks, S. L., Amaratunge, H.C., Are, J.R., Ayale, M., Banks, T., Bartailan, B., Banch, J., Binger, B., Blanksholl, B., Barkhailan, B., Banch, D., Barkel, F., Dani, H., Dalany, K.R., J., Barkel, F., Dalany, R.R., Delanoy, K.R., Daland, C., Dary, Carroll, L., Dalay, T., Dalhi, H., Doutharke, K.J., Barkel, F., Dalay, C., Barkel, F., Dalay, R., Daland, R., Barkel, F., Dalay, C., Barkel, F., Dalay, R., Barkel, F., Barkel

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INFORMATION: http://www.hgsc.bcm.tmc.edu/ or emailgc-help@bcm.tmc.edu
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES: STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts:

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences. Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:338-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found E.

http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

FEATURES

Location/Qualifiers

organism="Homo sapiens" /mol\_type="genomic\_DNA" /db\_xref="taxon:9606" /chromosome="3" clone="RP11-3J2" misc\_feature

. .2000 note="overlaps bases 38072. .40071 of clone AC125608"

/function="clone overlap" complement (1. .261) /rpf family="LiM4" complement (431. .913) /rpt\_family="LiME" repeat\_region repeat\_region repeat\_region

/rpt\_family="LIME"
complement(914. .1221)
/rpt\_family="AluSg"
complement(1222. .1808)
/rpt\_family="LIME" rpt\_family="L1ME" 454. .2811 'rpt\_family="L1N :omplement(2045. repeat\_region repeat\_region

/rpt\_family="THE1C" 2813. .3092 /rpt\_family="MLT11" 3194. .3870 repeat\_region repeat\_region repeat\_region

/rpt\_family="MSTD" [714. .4913 rpt family="AT rich":omplement(4297. .467 rpt\_family="L1PA3" 871. .3891 .3891 repeat\_region repeat\_region repeat\_region

/rpt\_family="AT\_rich"
complement (63377. .6630)
/rpt\_family="AluSx" rpt\_family="MLT11" 632. .5670 repeat\_region repeat\_region

/rpt\_family="L2" complement(14463. .17175) /rpt\_family="L1P" 17173. .18635 14620. 114933 / /rpt\_family="AluSg" complement(15183. 15254) family="LiPA16" ement (1005) /rpt\_family="LiPA15" complement(12819, .13533) /rpt\_family="L1" 13599. .13619 complement (10956. .11184) .12812) /rpt\_family="(TTTA)n"
complement(7094. .7374) /rpt\_family="AluSp" complement(7386..7695) 0024. .10387 /rpt\_family="blPAl6" /10388. .10417 rpt\_family="AT\_rich" 0637. .10675 family="AT\_rich" family="AT\_rich" family="L1M4" 1. 20130 family="L1ME" /rpt\_family="AluSx" 7910. .8035 family="L1PB1" /rpt\_family="AluSx" . .18635 family="L1PA7" /rpt\_family="L2" complement(12489. rpt\_family="MIR" family="L1" /rpt\_family="LiPH complement(10830 family="L2" /rpt\_famlly\_ 18793. .19462 /rpt\_family="L' .10818 .21073 .11658 /rpt\_fa 10754. 19461. repeat\_region repeat\_region

Length 112405; Score 560.2; DB 9; Pred. No. 1.4e-165; 38; 0; Mismatches Score 560.2; Query Match
Best Local Similarity 93.8%;
Matches 594; Conservative

CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAACTGTAAAACTA

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88.2%;
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Matches 582; Conserv
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DNA sequence and comparative analysis of chimpanzee chromosome 22

DNA sequence and comparative analysis of chimpanzee chromosome 22

La (bases 1 to 179114)

E 2 (bases 1 to 0.79114)

E 3 (bases 1 to 0.79114)

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E 1 - 7 - 22 Suchiro-chou, Taurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gec.riken.go.jp, URL:http://hgp.gec.riken.go.jp/

Tel:81-45-503-9111, Fax:81-45-503-9170)

The Chimpanzee Chromosome 22 Sequencing Consortium consists of:

*Chimpanzee Chromosome 22 Sequencing Consortium consists of:

*Chimpes National Human Genome Center at Shanghai, China;

*GBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute of Molecular Blotechnology, Jena, Germany; *KRIBB Genome Research
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Pan troglodytes chromosome 22 clone:RP43-179P23, map 22, complete
sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                Chemistry:
                                                     <u> ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG</u>
                                                                                                                                                     AGAGCACAGGGGGGGGGCACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                           541 CAACCCCTTTGGGTCCCCTCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center, Daejeon, Korea;
*Max-Planck-Institute for Molecular Genetics, Berlin, Germany;
*National Institute of Genetics, Mishina, Japan;
*National Institute of Genetics, Mishina, Tappan;
*National Yang Ming University Genome Research Center, Taipei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: Summary Statistics
Sequencing vector: pUC18, pUC13, pTZ19R; 100% of reads Chemistry
Dye-terminator Big Dye and ET; 100% of reads Assembly program:
Phrap; version 0.990329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN Genomic Sciences Center, Yokohama, Japan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178,810 bases at least Q40
263 bases at least Q30
35 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                    601 ATTAAATCTTGCAACTGAAAAAAAAAAAAA 633
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Center: RIKEN Genomic Sciences Center
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BSO00045.1 GI:37537312
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Consensus quality:
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                                                     421
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BS000045/c
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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Chitto://www.chori.org/bacpac/mchimp43.htm.
The clone may be obtained from Pieter J. de Jong and coworkers
(http://www.chori.org/bacpac).
VECTOR: baccai.e.
VECTOR: pastcai.e.
VECTOR: p
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                                                                                                                                                                                                                                                                                                                                                                                                                     The RPCI-43 chimpanzee BAC library was prepared from DNA isolated from the blood of a single male chimpanzee using published protocols (Osoegawa, K. et al. Genomics 52:1-8). The DNA from the chimpanzee ('Clint') was obtained from the Yerkes Primate Center in Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu, Kazutoyo Osoegawa, Evan Eichler & Pieter J de Jong. The library characteristics are described at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VECTOR: pTARBAC2.1
The PTB1 chimpanzee BAC library was prepared from DNA isolated from
cultured cells established from the blood of a single male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.gsc.riken.go.jp).
VECTOR: pKB145
The PTF22 chimpanzee Fosmid library was prepared from DNA isolated
from cultured cells established from the blood of a single male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 559.8; DB 9; Length 179114; Pred. No. 2e-165; 0; Mismatches 37; Indels 0; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clones may be obtained from Asao Fujiyama and co-workers (http://www.gsc.riken.go.jp).
VECTOR: pKS143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clones may be obtained from Asao Fujiyama and co-workers
                                                                                                                                                                           subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/chromosome="22"
/clone="RP43-179P23"
/clone_lib="RPCI-43 chimpanzee BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l. .1/9114
/organism="Pan troglodytes"
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Homo sapiens genomic DNA, chromosome 21q, section 18/105.
APO01674 AL163219 BA000005
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                          36710 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                  AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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     Score 556.6; DB 9;
Pred. No. 2.1e-164;
0; Mismatches 39;
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nilarity 93.7%;
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Best Local Similarity
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El (bases 1 to 114019)

El (bases 1 to 114019)

Elipipana, A., Yada, T., Totoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoda, Y., Watanabe, H. and Sakaki, Y. Homo sapiens 174,019 genomic DNA of 21q21.1-q21.2

Li Published Only in DataBase (2000)

E (bases 1 to 114019)

E Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Brityama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y. Direct Submission

E vilyama, A., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y. Direct Submission

Submitted (33-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato, Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@sec.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9923,
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * Genetics (addresses see below)

On May 30, 2000 this sequence version replaced gi:771721.

The chromosome 21 mapping and sequencing consortium consisting of * RIKEN Genomic Sciences Center, Human Genome Research Group, * Sagamihara, 228-8555, Japan.
Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and Yaspo, M.L.
The DNA sequence of human chromosome 21
Nature 405 (6784), 311-319 (2000)
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* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:

Info:genome@gbf.de

* URL: http://genome.gbf.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * Institute of Molecular Biotechnology, Genome Analysis, * Beutenbergstrasse 11, D-07745 Jena, Germany, * e.mail: gscj-submit@genome.imb-jena.de * URL: http://genome.imb-jena.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Max-Planck Institute for Molecular Genetics, Ihnestrasse 73, D-14195 Berlin, Germany, e.mail: info-chrzl@molgen.mpg.de URL: http://chrzl.rz-berlin.mpg.de/Li63219: submitted (10-Apr-2000).
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* e.mail: nshimizu@dmb-med.keio.ac.jp

* URL: http://www.dmb.med.keio.ac.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * e.mail: hattori@gsc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 149755)

Rattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 149,755 genomic DNA of 18q21

Leblished Only in DataBase (2000)

E (bases 1 to 149755)

Rattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Britori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Serica Submission

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                                   27381 CAACCCCCTTTGGGTCCCCTGCCTTTGTATGGGAGCTCTGTTTTCACTCTATTTCACTCT 27322
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                                                                                                                                                                                                                                                    AP001545 13-JUL-2000 Homo sapiens chromosome 18 clone RP11-762G24 map 18q21, WORKING DRAFT SEQUENCE, 13 unordered pieces.
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HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
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93.7%; Pred. No. 2.3e-164;
iive 0; Mismatches 39;
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146768 148219 contig of 1452 bp in length.
148320 149755 contig of 1456 bp in length.

* NOTE: This is a 'working draft' sequence. It currently
consists of 13 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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Score 551.8; DB 2; Length 149755; Pred. No. 6.8e-163;

86.9%; 91.8%;

Query Match Best Local Similarity

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152980)
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                                                                                                                                                                                                                                                                                                                                                   GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
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                                                                       67067 cccrorarchiraaccrocrigirachrigicrorrocagaarcaaacraaaacra
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                                                                                                                                              61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGGTGGACCC
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HTG; HTGS PHASE2; HTGS_FULLTOP; HTGS_CANCELLED.
Homo sapiens
Homo sapiens
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PRI 16-NOV-2001

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48688 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAGCTGTAAAACTA 48629
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DOE Joint Genome Institute.

Direct Submission

Submitted (31-AUG-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 163803)

DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 163803)
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                                                                                                                                                            48388 AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAACCTAGGTGGGAAGGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18268 ACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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Homo sapiens chromosome 5 clone RP11-405L7, complete sequence.
AC093531
                                                                                                                                                                                                                                  CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                                                                                                       GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
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                                                                                                                             CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngyven, C., Norbu, C., Norman, C. Peterson, K. O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K. O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K. Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M. Rieback, M. Rosetti, M., Sougnes, R., Schauer, S., Schueback, R., Seaman, S., Severy, P., Schauer, B., Stange-Thoman, N., Stojanovic, N., Strauss, N., Taylain, A., Talamas, J., Tesfaye, S., Thedore, J., Travers, M., Tavis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Zembek, L., Zimmer, A. and Zody, M., Tesfaye, S., Thedore, J., Zembek, L., Zimmer, A. and Zody, M., Taylain, N., Yasiliev, H., Viel, R., Vo, A., Zembek, L., Zimmer, A. and Zody, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Zembek, L., Zimmer, A. and Zody, M., J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., J., Young, G., Zainoun, J., Sember, J., Chang, J., Mihor, T., Mihor, J., Mihor, J., Marthews, C., Kanat, A., Kartas, A., Kartas, A., Kartas, A., Kartas, A., Kalta, J., Maylor, J., Noylor, C., Nogren, C., Noch, C., Norban, J., Roy, A., Schauer, S., Schubback, R., Seaman, S., Severy, P., Phunkhang, P., Pierre, M., Raymond, C., Retta, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stanger-Thomann, M., Scojanovick, N., Talamas, J., Viel, R., Woy, A., Schauer, S., Schubback, R., Tavers, M., Wassiliev, H., Viel, R., Woy, A., Wilson, B., Wu, X., Wyanan, D., Young, G., Zainoun, J., Viel, R., Woy, A., Wilson, B., Wu, X., Wyanan, D., Young, G., Zainoun, J., Spencer, B., Stanger-Thomann, M., Schauer, S., Seamen, S., Seamen, S., Sainet, A., Ecreen, Samite, A., Ecreen, Samite, A., Ecreen, C., Genome Canter, Mille
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consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

the accession number will be preserved.

Location/Qualifiers
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Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: 1.12582
Center clone name: 762_6_24
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/clone_lib="RPCI-11 Human Male BAC"
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Pred. No. 6.8e-163;
0; Mismatches 52;
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/morganism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="18"
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Best Local Similarity 91.8%;
Matches 583; Conservative (
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 176425) Sulston,J.E. and Waterston,R.

Toward a complete human genome Genome Res. 8 (11), 1097-1108

9847074

2 (bases 1 to 176425) Swearengen-Shahid, S., Meyer, R. and Dignan, G. The sequence of Homo sapiens BAC clone RP11-452N17 Unpublished (2001)

3 (bases 1 to 176425) Waterston, R.H.

Direct Submission

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Submitted (15-JAN-2002) Genome St
University School of Medicine, 44
M 63108, USA
4 (bases 1 to 176425)
Waterston, R.H.
Direct Submission
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www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.3.
Location/Qualifiers
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/mol_type="genomic DNA"
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Submitted (30-MAY-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (Dases 1 to 176425) Waterston, R.

Louis,

Washington

Sequencing Center, Washing 4444 Forest Park Parkway,

63108, USA

Materboun, ...
Direct Submission
Submitted (12-JUN-2002) Department of Genetics, Washington Submitted (12-JUN-2002) Department of Genetics, Missouri 63 University, 4444 Forest Park Avenue, St. Louis, Missouri 63 On May 30, 2002 this sequence version replaced gi:18640713.

Center code: WUGSC Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu

Center project name: H\_NH0452N17

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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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The clone sequenced to the left is RP11-624F4; the clone sequenced
to the right is RP11-362J3. Actual start of this clone is at base
position 1 of RP11-452N17; actual end is at base position 176425 of
                                                                                                                                                                                                                                                           SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Googawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
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RP11-452N17.
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PRI 12-JUN-2002 sequence.

linear I

7

Homo sapiens BAC clone RP11-452N17 AC107075

RESULT 20 AC107075/c DEFINITION AC107075.4 GI:21263352

ACCESSION VERSION KEYWORDS

sapiens (human)

Homo

ORGANISM

SOURCE

DNA

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

entire insert of this

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

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Polymorphisms exist between AC110086 and AC107075. Data from AC110086, AC116626 and AC018872 was used to finish AC107075. Location/Qualifiers
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                                  FEATURES
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/rpt\_family="Alu"
36767 .36809
/rpt\_family="AT\_rich"
37396 .37437
/rpt\_family="AT\_rich"
37816 .37850 // x16. .37850 //rpt\_family="A-rich" // 38954. .3937F rpt\_family="AT\_rich" 7693. .2784^ 40130. ..40216 /rpt\_family="L2" 41723. .42015 /rpt\_family="Alu" /rpt family="L1" 40130. 4001 rpt\_family="MaLR" 7499. .27532

9; Gaps Length 176425; Indels Query Match

86.9%; Score 551.8; DB 9;
Best Local Similarity 92.8%; Pred. No. 6.9e-163;
Matches 593; Conservative 0; Mismatches 37;

241 CATCAGCCAACCTCCCCAACAGCACTTGGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 300 . 160888 GAAATCTCAACTGCACCACTCATATGCCCCAGTTCAACAGGAAGCAGTTAGAGGGG

```
18040. 18346

/note="LiMEc repeat: matches 2106. .2409 of consensus"

18447. .18847. .1910 of consensus"

/note="LiMEc repeat: matches 1469. .1910 of consensus"

complement(18475. .18995)

/note="match: GSS: Em:AQ755181"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="LIPAS repeat: matches 5526. .6143 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="LIME3 repeat: matches 4094. .4381 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7552. 17740
note="LIMEc repeat: matches 2408. .2260 of consensus"
7741. 18039
note="AluSx repeat: matches 1. .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146. .8805
note="Ling repeat: matches 4381. .6140 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="LIM4 repeat: matches 2710, .3168 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     711. 15846
note="L1PA6 repeat: matches 11. .6143 of consensus"
5826. .16269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MER41B repeat: matches 114. .601 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20321. .20675
Notce="LTR16B repeat: matches 97. .464 of consensus"
20952. .21137
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=112 repeat: matches 2574. .2704 of consensus"
2290. .2509
/note=112 repeat: matches 2098. .2328 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MER5A repeat: matches 3. .186 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 64. .153 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="26 copies 2 mer aa 71% conserved"
23289. .23682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5826. .16269
note="L1M4 repeat: matches 3692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (4521. .5085)
/note="match: GSS: Em:AQ421033"
complement (4571. .5086)
/note="match: GSS: Em:AQ883615"
complement (4633. .5083)
/note="match: GSS: Em:AQ812769"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L2 repeat: matches 1693. . . 3497. .368 /note="MER20 repeat: matches 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:AQ881909"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="match: GSS: Em:AQ544837"
:085. .6174
                                                                                                                                                                                                                                                                                              Em: AQ704228"
                                                                                                                                                                                                                                            'note="match: GSS: Em:AQ609536"
                                                                                                                                                                                                                                                                                                                                                                                               /note="LTR5 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                Em: B75711"
                                                                              /mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
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                  location/Qualifiers
                                                                                                                                                                                                                                                                                              'note="match: GSS:
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Submitted (105-WAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Nov 20, 2000 this sequence version replaced gi:11125403.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw.: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
thttp://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
IMPORTANT: This sequence is not the
sequence This sequence is not the
sections only once, except for a 100 base overlap.
The true left end of clone RPI1-12B13 is at 1 in this sequence. The
true left end of clone RPI1-12B13 is at 128369 in this sequence.
The true right end of clone RPI1-13B13 is at 128369 in this
sequence. This sequence was finiahed as follows unless otherwise
noted all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., phred
quality >= 30; an attempt was made to resolve all sequenced by at least one plasmid subclone or more than one MI3
subclone; and the assembly was confirmed by restriction digest.
RIII-12B13 is from the library RFCI-11: constructed by the group
problems, such corrigines between
                                                                                                                                                                                  160648 GGAGAGCTCACTAAATGCTAATTAGGCAACAACAAGAGGGTAAAGAAATAGCCAATCACC 160589
                                                                                                                                                                                                                                                                                                                                                                                       160768 AGGACTAGCTGGATTTCCTAGGCCGACTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACC 160709
                                                                                                   160708 GCTTCCATCTTTAAACACGGGCTTACAACTTAACTCACATCACATCAGATAGTAA 160649
                                                                                                                                                                                                                                                                                      AL139090 128468 bp DNA linear PRI 12-APR-2001
Human DNA sequence from clone RPI1-12B13 on chromosome 6 Contains
STSs and GSSs, complete sequence.
                                                                                                                                                                                                                                                         531
                                                                                                                                                                                                                                                                                                                                                          591
                                                    GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCA----- 412
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Catarrhini; Hominidae; Homo.
                                                                                                                                                     413 -GAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC
                                                                                                                                                                                                                                                      472 TATTGCCTGAGAGCACACGGGAGGACAAGGATCGGGATATAAAACCCAGGCATTCGAGC
                                                                                                                                                                                                                                                                                                                                                          CGGCAACGGCAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160468 CTTCACTCTATCAAATCTTGCAACTGCAAAAAAAAAAA 160430
                                                                                                                                                                                                                                                                                                                                                                                                                                                              592 TITCACTCTATTAAATCTTGCAACTGAAAAAAAAAAA 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 128468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL139090.11 GI:11228536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garner, P.
Direct Submission
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KEYWORDS
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ORGANISM
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AL139090/c
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AUTHORS
TITLE
JOURNAL
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.188 of consensus"

.2089 of

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.1377 of consensus'

.4135 of consensus"

.6184 of consensus"

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/// / mote="LilM4 repeat: matches 2266. .2691 of consensus" 44140. .44339 // note="LilM4 repeat: matches 6093. .6289 of consensus" 46709. .47216 // note="LilM8 repeat: matches 5588. .6169 of consensus" 47217. .47431 // note="LilM4 repeat: matches 4637. .4856 of consensus" 47487. .47439 // note="LilM4 repeat: matches 8. .345 of consensus" 47487. .47839 // note="LilM4 repeat: matches 8. .345 of consensus" // note="LilM4 repeat: matches 4451. .4645 of consensus" 48031. .48031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="LTR17 repeat: matches 257. .780 of consensus"
10490. .41321
Inote="LINE3A repeat: matches 5261. .6131 of consensus"
11354. .41655
Inote="Alway repeat: matches 1. .302 of consensus"
11971. .42279
                                                                                                                                                                                                                                                                                                                                                                                                                                      13151 ... 13174 ... 1001es 2 mer tt 95% conserved" ... 12 copies 2 mer tt 95% conserved" ... 1376 ... 13779. ... 138791 ... 137717 repeat: matches 8244 ... 8523 of consensus" ... 131791 ... 13137 ... 138137
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19436    .50712
"note="LiMD2 repeat: matches 5056. .6333 of consensus"
complement (50811. .51360)
note="matches" GSS: Em: Ap536659"
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3366. .43774
                                                                                                                                                                                                                  73482. .26261

Anote="LiPA3 repeat: matches 5. .776 of consensus"

86257. .31504

16614. .32312

Anote="LiPA4 repeat: matches 3918. .4608 of consensus"

Anote="LiPA4 repeat: matches 3918. .4608 of consensus"
                                                                                                                                                                                                                                                                                                                                             2398. 32850
note="LIM4 repeat: matches 4626. .4909 of consensus"
12799. 32963
'note="FRAM repeat: matches -2. .162 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7746. .57868
note="MER33 repeat: matches 202. .323 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="HERV17 repeat: matches 1. .1836 of consensus" 1958. .40489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .727 of consensus"
                                                                                                                  consensus"
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6710. .57178
note="MLTIC repeat: matches 1. ,463 of consensus"
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8890. .59200
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3255. .43365
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                              consensus"
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8555. .58752
                              matches 90.
                                                                        Em: AQ027280'
23421. .23472
/note="MIR repeat: m
24395. .24791
                                                                      note="match: GSS:
4638. .24848
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Catarrhini, Hominidae, Homo.
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Submitted (14-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                            421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATTGCCTG
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         59956. .60646
/note="match: GSS: Em:B82923"
61550. .61582
/note="LIME2 repeat: matches 6133.
61583. .62103
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                                                                              Query Match 86.8%; Score 551.4; DB 9; Best Local Similarity 93.9%; Pred. No. 8.8e-163; Matches 596; Conservative 0; Mismatches 36;
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On Jul 17, 2001 this sequence version replaced gi:13751261.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accessation numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; We:, NORMPEP; Information on the WORMPEP; LELLOWING ADDITION or and other source databases: Em:, EMBL; Sw:, Charles of the contract of the contraction on the WORMPEP; LELLOWING and the contract of the contraction on the WORMPEP there are not the contraction and the contractions are used to associate primary and the contractions are used to associate primary as a compression on the WORMPEP. The contraction on the WORMPEP there are not the contraction and the cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 happing Group. Further information can be found at http://www.sanger.ac.uk/HGF/Chhi3 RP11-456B18 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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note="LTR1 repeat: matches 675. .785 of consensus"
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'note="LOR1a repeat: matches 1. .497 of consensus"
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1059. .8292
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                requests: clonerequest@sanger.ac.uk
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/mol_type="genomic DNA"
/db xref="taxon:9606"
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/clone="RP11-456B18"
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note="LTR29 repeat:
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note="MER4D repeat:
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1. .140756
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/note="17 co
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                                                 COMMENT
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note="MSTC-internal repeat: matches 2. .1651 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="LIMC4 repeat: matches 6629. .7089 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .6540 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thote="Limb2 repeat: matches 5745. .6199 of consensus" note="Limb2 repeat: matches 5277. .5594 of consensus" note="Limb2 repeat: matches 357. .625 of consensus" note="Limb3 repeat: matches 357. .625 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 5400. .6155 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 4726. .5242 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .354 of consensus"
                                                                                                                                                                                                                                                                                                                                      'note="MER54B repeat: matches 585. .789 of consensus"
                                                                                                                                                                                                                                                                                                                                                                            note="MER54B repeat: matches 112. .278 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           matches 283. .341 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1645, .21984 matches 55. .393 of consensus 2081. .22583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8120. .19291
note="LIP repeat: matches 1726. .2897 of consensus"
                                                                                                                                               /note="MER4D repeat: matches 396. .973 of consensus"
12852. .13221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MER66A repeat: matches 163. .478 of consensus 16903. .17014
/note="MER54B repeat: matches 3. .115 of consensus" 17195. .17491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Alusx repeat: matches 20. ,311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3498. .23784
note="AluJD repeat: matches 1. .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .394 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matches 1. .295 of consensus"
                                                                                                                                                                                                                                                                                  4799. .15173
note="THE1B repeat: matches 1. .364 of consensus"
6144. .16346
                                                                                                                                                                                                                                                                                                                                                                                                                     note="MER66A repeat: matches 1. .69 of consensus"
6570. .16629
  .151 of consensus"
                                                                                                               note="MER4D repeat: matches 1. .234 of consensus"
[2164. .12767
                                                                                                                                                                                             matches 1. .364 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MIR_repeat: matches 31. .238 of consensus" 5404. .25696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 1. .405 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="AluY repeat: matches 1. .297 of consensus"
                                                                              consensus,
                                                                                                                                                                                                                                     /note="THE1B-INTERNAL repeat: matches 1. .1580 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="25 copies 5 mer atttt 62% conserved"
9686. .19745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tg 95% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   copies 2 mer ta 79% conserved"
                                                                              .144 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER61A repeat: matches 160. 31648. 31785 / Note="L1MC4 repeat: matches 6409. 31813. 33243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="12 copies 5 mer tttaa 71%
                                        'note="MER67D repeat: matches 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 30.
repeat: matches 2.
                                              11249, .11332
/note="MIR repeat: matches 69.
11923, .12159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="12 copies 2 mer
0688. .30874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MER41B repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3873, .24169
note="AluSg repeat:
5044, .25238
                                                                                                                                                                                                  /note="THE1B_repeat:
13222. .14798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :5832. .26218
note="MSTC re
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23498. .23784
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note="L1PB2 r
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Exercises 1 to 16/36b)

Adderson, S., Baldwin, J., Barna, N., Beckerly, R., Béda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Béda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Béda, F., Anderson, S., Baldwin, J., Boukhgalter, B. Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Mardulad, J.C., Johnson, R., Jones, C., Liu, G., Locke, K., McPheeters, R., Meldrim, J., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., McBwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., McBwan, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Storianovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Zimmer, A. and Zody, M.

Direct Submission

All repeats were identified using RepeatMasker: html

Lepeats were identified using RepeatMasker: html

Lener: Mair Show & Storen, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html

Lener: Whitshead Institute/ MIT Center for Genome Research

Center: Whitshead Institute/ MIT Center for Genome Research
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Homo sapiens clone RP11-13C18, WORKING DRAFT SEQUENCE, 10 unordered
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Unpublished
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18708. .48806
/note="AluJo/FRAM repeat: matches 197. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
                                                                                                                                                                                                                                                                                                                                      .6152 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                              41279. .41308
/note="15 copies 2 mer aa 86% conserved"
4274. .42933
/note="LiMAS repeat: matches 6064. .6256 of consensus"
42973. .43275
/note="AluSx repeat: matches 1. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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                                                                                                                                                                             34465. .34825
/note="THB1C repeat: matches 1. .360 of consensus"
/note="THB1C repeat: matches 202. .403 of consensus"
/note="MER67C repeat: matches 202. .403 of consensus"
/note="LiPA12 repeat: matches 6076. .6152 of consensus
/40953. .41258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .448 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52250. .52349
Thote="MIR repeat: matches 131. .228 of consensus"
57636. .52996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="THEIC repeat: matches 1. .370 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="Alusg repeat: matches 1. .293 of consensus"
                                          /note="THELC repeat: matches 1. .371 of consensus"
32824. .34464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MLT2B repeat: matches 2. .399 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                 note="AluY repeat: matches 1. .308 of consensus"
                                                                                                                     'note="THE1C-internal repeat: matches 3. .1651 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 140756;
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/note="L1MEc repeat: matches 2274. .2369 of
50637. .50927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 551.4; DB 9; Length
Pred. No. 8.9e-163;
0; Mismatches 31; Indels
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/note="match: STS: Em:HSPH07E5"
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ilarity 94.3%;
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                                              NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Insert size: 166466; sum-of-contigs
Quality coverage: 4.8 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                       1372: contig of 1272 bp in length
1372: gap of 100 bp
4088: contig of 2716 bp in length
4188: gap of 100 bp
6500: contig of 2312 bp in length
6600: gap of 100 bp
15485: contig of 2312 bp in length
15585: gap of 100 bp
27637: contig of 12052 bp in length
27637: contig of 1222 bp in length
39588: contig of 1221 bp in length
40058: gap of 100 bp
54618: gap of 100 bp
82725: contig of 28007 bp in length
54718: gap of 100 bp
82725: contig of 28007 bp in length
123322: gap of 100 bp
123222: contig of 44047 bp in length
16336: contig of 44034 bp in length
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/organism="Homo sapiens"
/organism="Homo sapiens"
/mol type="genomic DNA"
/db Xref="taxon:9606"
/clone="RP11-13C18"
/clone="RP11-13C18"
/locte="RPCI-11 Human Male BAC"
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/note="assembly_fragment"
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/note="agsembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission

Direct Submission

Submitted (18-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

On Oct 5, 2001 this sequence version replaced gi:15962724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 AGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                                                                                                                                                                                                                                                361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGGGCCAATCAGAGGTC
                                                                                GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
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Homo sapiens chromosome 13 clone RP13-276D12.
AL607153
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Contact: humquer/@sanger.ac.uk
Contact: humquer/@sanger.ac.uk
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Homo sapiens (human)
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164211 bp DNA linear HTG 13-JUL-2000
HOMO sapiens chromosome 18 clone RP11-732P12 map 18q21, WORKING
AP002790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                          Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Published Only in DataBase (2000)

2 (bases 1 to 164211)

2 (bases 1 to 164211)

Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Contact: Project Information
Center project name: Humbraft18
Center project name: RR11-732P12
Center clone name: RR11-732P12
Center clone name: RR11-732P12
Center clone name: RR11-732P12
Center project name: RR11-732P12
Center
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Consensus quality: 154344 bases at least Q40
Consensus quality: 159150 bases at least Q30
Consensus quality: 159100 bases at least Q30
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Homo sapiens (human)
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                 RESULT 25
AP002790/c
                                                                                                                       DEFINITION
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12224 GABATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCAGGAAC----AGAGCAGT 12279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12280 CATTGGCCAACTTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 12339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12164 CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATCGAAGGCACCCCTCCTGAG 12223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                              * NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

I 183499: contig of 183499 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
Insert size: 179011; 5.6% error; agarose-fp
Quality coverage: 12.84x in Q20 bases; sum-of-contigs Quality
coverage: 13.23x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 183499;
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Pred. No. 9.4e-163;
0; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
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94.3%;
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Best Local
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CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
          /note="assembly_fragment_clone_end:SP6_vector_side:left"
138847. .143265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGACCGGCCTGCTAGCCCCATGCTCAATGACATTGAAGGCACCCCTCCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 550.2; DB 2;
Pred. No. 2.2e-162;
0; Mismatches 53;
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150443, 153002-
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143366. 147643
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162822. .164211
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

Best Local Similarity 91.7%;
Matches 582; Conservative
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      NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                        153102: contig of 2560 bp in length 153102: gap of 100 bp 15324: contig of 2122 bp in length 15225 contig of 2122 bp in length 15225 contig of 1243 bp in length 15525 contig of 1243 bp in length 15568 l56567: contig of 106 bp 1568 l5667: gap of 100 bp 1568 l5667: gap of 100 bp 15832: contig of 106 bp 15832: contig of 106 bp 171 bp in length 15832: contig of 2478 bp in length 16243: gap of 100 bp 171 bp in length 16272: contig of 2478 bp in length 1724 l6272: contig of 2478 bp in length 1722 l6282: gap of 100 bp 1722 l6282 l6
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Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasilliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                          Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 30, 2002 this sequence version replaced gi:21700673. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence submissions@genome.wi.mit.edu
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Baldwin, J., Barna, N., Bastran, V., Beda, F.,

Boguslavkiy, L., Buckleglter, B., Brown, A., Burkett, G.,

Campoplano, A., Cascle, A., DeArellano, K., Dewar, K., Diaz, J.S.,

Dodge, S., Domino, M., Doyle, M., Ferreira, F., FitzHugh, W., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Rowland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Klein, J., LeaNcoque, K., Lamazares, R., Landers, T., Lehoczky, J.,

Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,

McCarthy, M., McEwan, P., McGwer, R., McKernan, K., McDheeters, R.,

Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,

Nowell, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,

Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,

Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Voung, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
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Universe Submitted (122-8000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

1 (bases 1 to 167843)

2 (bases 1 to 167843)

2 Sirren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Rarata, P., FitzGerald, M., Gage, D., Galagan, J., Rarata, A., Kells, C., Linde, F., Johnson, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Micol, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Micol, R., Matthews, C., Murphy, T., Naylor, J., Merus, B., Micol, R., Norbu, C., Norman, C., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Seenen, K., Senen, S., Schubc, S., Schubc, S., Schubc, S., Schubc, S., Senen, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zamber, J., Sane, J., Schubc, J., Wuxa, Wayman, D., Young, G., Zainoun, J., Sene, L., Zimmer, A., and Zody, M.

Direct Submission
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Submitted (06-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 167843)

S Birren, B. Nubbau, C. Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nubbau, C., Lander, E., Chepel, Y., Collymore, A., Camarata, J., Chang, J., Chazaro, B., Chepel, Y., Collymore, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Perreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Lindblad, Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
                                                              ACUDEBUL 167843 bp DNA linear PRI 30-JUL-2002
Homo sapiens chromosome 18, clone RP11-120K19, complete sequence.
AC064801
                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 167843)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-120K19
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                                                                                                                                                                                                                               Homo sapiens (human)
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AL121784
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1 (bases 1 to 186523)

1 (bases 1 to 180523)

Brottier, P., Cattolico, U., Dasilva, C., Robert, C., Wincker, P., Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C., Sqyay, G., Saurin, M. and Weissenbach, J.

Sequencing of the human chromosome 14

Unpublished

2 (bases 1 to 180523)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope.

Direct Submission
Submitted (01-AUG-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Aug 23, 2001 this sequence version replaced gi:12001714.
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                                                                       421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                                                                                                                                                                                        481 AGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                          CAACCCCCTTTGGGTCCCCTTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
                GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                                                                                                                                        GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGACCAATCAGAGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap; version 2.0 Quality coverage: 7.78x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL121784.5 GI:15282089
HTG; HTG; ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
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complement (21102. .21388)
/rpt family="AluJo"
21410. .2169
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                            /rpt_family="MER50"
complement (14240. .14530)
/rpt_family="Aludo"
14881. .1528
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complement(15654. 15794)
frpt_family="MERSA"
15935. 16489
/rpt_family="MLT2A2"
                                                                                                                                                                                                        29557. .29579
/rpt family="(GAAAA)n"
complement(29806. .30079)
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complement(19903, .20
                                                                                                 /rpt_family="LTR16A1"
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21693. 21985
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21986. 22149
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5031. .25348
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29217. .29290
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/rpt family="MLT1C"
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/rpt_family="AluY"
complement(28729. .
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2512. .13031
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Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D. and Hood, L.
Sequencing of human chromosome 15 D15S146-D15S117 region Unpublished

2 (bases 1 to 190565)
Rowen, L., Madan, A., Qin, S., Abbasi, N., Dors, M., Dickhoff, R., Shaffer, T. and Hood, L.
Shaffer, T. and Hood, L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (25-ARR-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA 3 (Dases I to 190565) Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Barke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, R., Pate, D. and Hood, L.
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Homo sapiens chromosome 14 clone RP11-325L17 map 14q31, complete
sequence.
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Submitted (27-MAR-2001) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
98105, USA
On Mar 27, 2001 this sequence version replaced gi:8247780.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                 421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                481 AGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
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Center: Multimegabase Sequencing Center
Center: Code: UNMSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen@systemsbiology.org
Contact: Leerowen@systemsbiology.org
Contact: Leerowen@systemsbiology.org
Contact: Summary Statistics
Sequencing vector: pGC18; LO8752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
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/map="14q31"
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985. .1035
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/db_xref="taxon:9606"
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Human chromosome 14 DNA sequence BAC C-2547L24 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiquenave, F., Every, M., Brchenberg, R., Brulls, T., deBerardinis, V., Cruaud, C., Gyapa, G., Saurin, W. and Weissenbach, J. Seguencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-MAY-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
on Jun 3, 2000 this sequence version replaced gi:7406569.
                                     540
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Downstream BAC (overlapping the SP6 end) : R-895M11 (AC=AL133153)
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 203777) ......... Pobert. C. Wincker, P.
                                                      AGAGCACAGCGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                      CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
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مه
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Genoscope / Centre National de Sequencage
Center code: GS
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Location/Qualifiers
                                                                                                                               23557 CTACCCTCTTTGGGTCCCCTCCCTTTGTATGGGAGCTCAGT
                                                                                                                                                                                             23607 ATTAAATCTTGCAACTGCAAAAACAAACAAACAAA 23641
                                                                                                                                                                          635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.genoscope.cns.fr/
Contact: SegRef@genoscope.cns.fr
                                                                                                                                                                          /organism="Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
2 (bases 1 to 203777)
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Range : bases
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Direct Submission
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/note="low quality data"
110860. .110875
/note="low quality data"
/note="low quality data"
/note="low quality data"
/note="low quality data"
/note="single clone coverage. PCR and transposons tried."
117677. .117680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 300
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larity 92.9%; Pred. No. 5.4e-162;
Conservative 0; Mismatches 35;
        /note="low quality data"
3865. 3870
/note="low quality data"
14875. 14880
/note="low quality data"
17060. 17095
/note="low quality data"
17488. 17588
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17730. .117748
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.44847. .144850
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/note="low quality data"
19433
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46474. .46580
/note="low quality data"
46695. .46700
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18505. .118736
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es 590; Conserv
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Db 9913 ACTANAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCGCCTG 9854  Qy 481 AGACCACGCGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGCAACGG 540  Db 9853 AGACCACAGCAGGACGACAATGATCGGGATATAAACCCAGGCATTCGAGCCAACGA 5794  Qy 541 CAACCCCTTTGGGTCCCCTCCTTTGTATGGGCGCTCTTTTCATTCTCTCT 600	RESULT 30 AC109992 LOCUS AC109992 DEFINITION HOMO Sapiens 3 BAC RP11-383G6 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	ACCESSION AC109992 VERSION AC109992.6 GI:21591818 KEYWORDS HGG SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE I (bases I to 112544)	AUTHONS MUZIN, U.W., AddamB.L., AMID-CHOLDIA, D., APYLL, MALT-DAMBA, BARKS, T. Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, M., Davis, C., Davy-Carroll, L., Dederich, D., Bavis, C., Davy-Carroll, L., Dederich, D., H. H.	Detandy, N. N., Detagon, V. Detan, Nocha, S., Durbin, K.J., Douthwaite, K.J., Draper, H., Dugan, Nocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Healton, K., Hernandez, J., Hernandez, O., Hodgon, A., Hogues, M., Holloway, C., Hollows, M., Howei, R., Howel, S., Hume, J., Huns, J., Huns, M., Huns, J., Huns, J., Hune, J.,	Jackson, L. B. Jacobson, B. Jia, Y. Johnson, R., Jolivet, S., Jackson, L. B., Jacobson, B., Kelly, S., Khan, U., King, L., Korvah, J., Kovat, C., Kratcovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L., Lewis, L., Li, Z., Lichterge, O., Lideu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindel, A., Matzier, Massey, E., Mawhiney, B., McLeod, M. P., Meador, M., Mela, G., Metzker, M., Miner, Z., Mitchell, T., Mohabbat, K.,	Moore, S., Morgan, M., Moorlsh, Y., Morrish, S., Moser, M., Neatson, S., Morgan, M., Newtson, J., Newtson, N., Nguyen, A., Moyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pacc, A., Payton, B., Peerry, J., Peerry, J., Perers, I., Payton, B., Ren, Y., Rives, M., Pickens, R., Primus, E., Pulte, M., Ruiz, S., Savery, G., Scherer, S., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Sonaike, T., Sparke, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tang, H., Stone, H., Sturch, J., Taylor, C., Tabor, P., Tang, H., Tansey, J., Taylor, C.,	Taylor, T., Telfrod, B., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, K., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstock, G. and Gibbs, R. Direct Submission  TITLE Direct Submission  JOURNAL Unpublished  REFERENCE 2 (bases 1 to 112544)
/mol_type="genomic DNA" /db_xref="taxon:9606" /cb_mosome="14" /clone="14" /clone="14" /clone="15-7247L24" /clone="c-2547L24" /clone="deltarech-D" 9045: -9369 dbsTs:STS-5054886 Identified using the e-PCR software (G. Schuler)" 1662816834 /note="matching BMBL:G20331 RHdb:RH16802 dbsTs:STS15337 dbsTs:STS13337	Identified using the e-PCR software (G. Schuler)" 4237942560 /note="matching EMBL:N80119 RHdb:RH46446 dbSTS:STS:STS:STS:STS:STS:STS:A using the e-PCR software (G. Schuler)"	9 EMBL:T02957 19 EMBL:T02957 10 the e-PCR software (G. 9) 9 EMBL:R51241	RHdb:RH53819 dbSTS:STS42905 Identified using the e-PCR software (G. Schuler)" 167890. 168003 Note="matching EMBL:G38628 RHdb:RH97597 RHdb:RH97597 RHdb:RH938060 GbSTS:G7859195 Identified using the e-PCR software (G. Schuler)"	IGIN  Query Match  86.5%; Score 549; DB 9; Length 203777;  Best Local Similarity 92.9%; Pred. No. 5.5e-162;  Matches 590; Conservative 0; Mismatches 35; Indels 10; Gaps  1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA	Db 10333 CCCTTTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCTGGAATCAGAATCAGAACTA 102/4  Qy 61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120  Db 10273 CAAATAGTTCTTCAAATGGAGCCCCAGATGACTCATGACTAAGATCTACCATGACCC 10214  Qy 121 CTGGACCGCCTGCTAGCCCATGGTCCGATGATAATGACATCAAGAGCCCCTCCCGAG 180  Db 10213 CTGGACCGGCCTGCTAGCCCATGATTAATGACATCAAGGCACCCTCCCGAG 110  TOTALAACAGCGGCCTGCTAGCCCCATGTTCATTAATGAACATCAAGGCACCCTCCCGAG 110  TOTALAACAGCGGCCTGCTAGCCCCATGTTCATGATGTTAATGAACAACAAACA	181 10153 . 241	Oy 301 AGACTAGCTGGATTTCCTAGGCCAACGAAGATCCCTAAGCCTGGCGGAAGGTGACT 360

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DB 9; Length 112544;
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complement(19530. .20155)
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complement(20156. .20458)
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complement(20459. .20559)
/rpt_family="L2"
.20687. .20790
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complement(2622. .2786)
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complement'/"""
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complement(11215. 11374)
rpt family="U1"
complement(11387. 11681)
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complement (7505. 7618)
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6389. .6551
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complement(7206. 7491)
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complement(3135. .3392)
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5391. .5415
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| 13076. .13361
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complement(5509. .580
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/rpt_family="MADE1"
11176. .11213
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1217. .21344
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omplement (15115.
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6981. .7109
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22410. .22545
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2173. .12203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STSB are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the BST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission

Direct Submission

Submitted (12-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA

On Jun 26, 2002 this sequence version replaced gi:20976483.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                 Submitted (26-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 112544)
                 Direct Submission
Submitted (09-FEB-2002) Human Genome Sequencing Center, Department
Cobmitted Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
(bases 1 to 112544)
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                                                                                                                                                              Center, Department
of Medicine, One
                                                                                                                                                     Submitted (18-MAY-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA (bases 1 to 112544)
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/rpt family="LiM4"
complement (1499. .1804)
/rpt family="AluGa"
complement (1805. .2516)
/rpt_family="LiM4"
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/organism="Homo sapiens"
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/chromosome="3"
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                                                                                                                                                                                                                                                                     Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-AUG-1999) Whitehead Institute/MIT Center for Submitted (22-AUG-1999) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 10, 2000 this sequence version replaced gi:7229764. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
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7749: gap of 100 bp
9020: contig of 1271 bp in length
9120: gap of 100 bp
10798: gap of 100 bp
12208: contig of 1578 bp in length
12308: contig of 1410 bp in length
12308: gap of 100 bp
46811: contig of 34503 bp in length
46911: gap of 100 bp
192178: contig of 145267 bp in length
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Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center project Information
Center project name: L1480
Center clone name: 11.20
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-1L20"
/clone="RP71"
1 7649
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12309. .46811
/note="assembly_fragment"
46912. .192178
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clone_end:SP6
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7750. .9020
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Homo sapiens clone RP11-1L20, WORKING DRAFT SEQUENCE, 6 unordered
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Bakren, B., Linton, L., Bardain, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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                                                                                                                                                                                                                                                                                                                4108 CAAATCGTTCTTCAAATGGAGCCCCAGATGCAGTCCATGACTAAGATCTACGGGGGGGCCC
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                                Pred. No. 1.2e-161;
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HTG; HTGS PHASE1; HTGS_DRAFT.
HOmo sapiens (human)
Homo sapiens
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                             llarity 92.4%;
Conservative
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                                    Local Similarity
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                                                        : segref@genoscope.cns.fr
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                       Direct Submission
Submitted (30-APR-2001) Genoscope - Centre National de Seq
Bp 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscop
- Web : www genoscope.cns.fr)
On May 2, 2001 this sequence version replaced gi:13449984.
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Pred. No. 1.5e-161;
0; Mismatches 39;
                                                                                                                                    Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SegRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="14"
/clone="R-784H12"
/clone_lib="RFCI-11"
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llarity 93.4%;
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Human chromosome 14 DNA sequence BAC R-784H12 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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llarity 93.4%; Pred. No. 1.5e-161;
Conservative 0; Mismatches 39;
    /note="assembly_fragment
clone_end:T7
vector_side:right"
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15297 CACTAMANTGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATGCCT 15356
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Homo sapiens BAC clone RP11-809C23 from 2, complete sequence.
AC068492
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Submitted (09-MAY-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 172281)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-OCT-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On May 9, 2001 this sequence version replaced gi:7677994.
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Submitted (02-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 172281)
Waterston,R.
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Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                           GAGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTTCGAGCCGGCAACG
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                                                                CACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCT
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Center code: WUGSC
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The sequence of Homo sapiens BAC clone RP11-809C23
Unpublished (2001)
3 (bases 1 to 172281)
Waterston, R.H.
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Contact: sapiens@watson.wustl.edu
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Genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Waterston, R.
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Center project name: H\_NH0809C23 ----- Summary Statistics

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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhoo, B., Frengen, B., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                 This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-809C23;
actual end is at base position 172281 of RP11-809C23.
Location/Qualifiers
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1872. 3997
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9485. .9630
/rpt_family="MaLR"
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161. _1218
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**Gaps** 

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169418 bp DNA linear PRI 31-MAY-2002
Homo sapiens chromosome 3 clone RP11-66G8, complete sequence.
AC104163 AC073868
AC104163.2 GI:21281541
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2 (bases I to 169418)
2 (classes Losses) W.V., Raymond, C. and Haugen, E.D. Direct Submission
                                                                                                                        CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGACTGAGAGAC 300
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 169418)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                                                                                                                                                                        CIGGACCGGCCTACCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                         181 GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
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                                                                            Indels
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Pred. No. 1.7e-161;
0; Mismatches 46;
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                                                     86.2%;
ilarity 92.4%;
Conservative
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JOURNAL REFERENCE AUTHORS

TITLE JOURNAL COMMENT

3814 3835 8434 8627 512 <800 4550 4514 174 <800 449 <800 13599 13502 3671 3186 3034 1967 2060 1165 1179 1119 1142	6886 2248	<pre>&lt;800 990 982 11650 1 1860 10194 10069 9162</pre>	214 <800 7207 6886 3337 3297 4500 4514 6300 6210 1749 1637	4632 4514 66 <800 704 <800 704 <800 704 <800 704 <800 704 <800 704 <800 704 <800 704 <800 704 704 <800 704 704 <800 704 704 704 704 704 704 704 704 704 7	305 <800 6827 6886 3500 3500 3843 3835 8122 8155 239 <800	<800 1177 1179	1455	1179 3938	4849 1857	3835 4583 4553 2804	1681 1613 6464 6479 1955 1918 	897 898 2362 2418 195 <800 4602 4514 2046 2051 7172 7125	2839 2875 6729 6886 1173 1142 649 <800 2952 2916 1572 1637	2131 2060 1712 1683 514 <800 2302 2318 309 <800 2058 2116
Submitted (05-DEC-2001) Genome Center, University of Washington,  Box 352145, Seattle, WA 98195, USA  (bases 1 to 169418)  Sauth, R.K., Olson, W.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,  Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.  and Haugen, E.D.  Direct Submission  Direct Submission  Conversity of Washington.	 Web site: http://www.genome.washington.edu Conteact: uwgettgs@u.washington.edu Drafting Center: WUGSC	Center project name: chr-3 Center clone name: RP11-66G8 (bc0186) Summary Statistics Sequencing vector: unknown; 62% of reads Sequencing vector: plasmid; L08752; 38% of reads	Chemistry: Dye-terminator ET; 66% of reads Chemistry: Dye-terminator Big Dye; 34% of reads Assembly program: Phrap; version 0.990319 Chemistry: Dye-terminator Big Dye; 34% of reads	Consensus quality: 169408 bases at least Q30 Consensus quality: 169418 bases at least Q20 Consensus quality: 169418 sum-of-contige Insert size: 169418; sum-of-contige	Oualley coverage: Iz.zx in \( \text{in \( \text{Lorenzy} \) \) \) \) \) \( \text{Coverage} \) \) \( \text{In \( \text{Lorenzy} \) \) \) \( \text{Coverlapping Sequences} \) \( \text{Sequences} \) \( \text{Soverlap} \) \( \text{System} \) \(	5: KFII-1953D3 (UNGC:DCV129) ALIOHIO, 7009 DF COLLEGE Sequence Quality has been annotated with sequence quality Afric entry has been annotated with sequence quality actimates commuted by the Phran Assembly Drogram.	All manually edited bases have been reduced to quality zero.  Quality levels above 40 are expected to have less than  1 error in 10,000 bp.  Base-by-base quality values are not generally visible from the  GenBank flat file format but are available as part	This sequence was finished as follows unless otherwise noted:  all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing		Sequence Validation: This sequence has been validated by Multiple Complete Digest fingerplinting. Comparison of the experimentally derived digest fingerplinting. Comparison of the experiments is given below.	The decrease with sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp)	are not resolved in the fingerprint and hence do not appear	SeqDerMap FngrPrnt SeqDerMap FngrPrnt	8696 8873 8104 8155 459 <800

OY 481 AGAGCACAGCGGAGGACAAGATCAGGATATAAACCCAGGCATTCGAGCCGCAACGG 540	RESULT 35 AC10444 LOCUS AC10444.2 GI:20198585 AC10444.2 GI:20198585 KEYWORDS KEYWORDS ROMANISH HTG. SOURCE HOMO sapiens (human) CRGANISM HOMO sapiens LOCUS	Direct Submitted Submitted Box 352145 3 (bases) Kaul, R.K., Saenphimma Direct Submitted Box 352145 On Apr 19, Center Center Center Web sip	Contact: uwgchtgs@u.washington.edu
3854 2860 6059 2332 6462 3500	1369 <800 15508 1240 <800 3500	); Gaps 1; AAACTA 60        AAACTA 160456	redaccc 120
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Direct Submission
Submitted (26-ARR-2001) Genoscope - Centre National de Sequencage :
BP 19106 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Apr 2, 2001 this sequence version replaced gi:13016608.
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Human chromosome 14 DNA sequence BAC R-21A20 of library RPCI-11
AL390799
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(Dasea 1 to 16924)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,

Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,

Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,

Gyapay,G., Saurin,W. and Weissenbach,J.

Sequencing of the human chromosome 14

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1998 CAACCGCCTTTGGGTCCCTTCTATGAGAGCTCTGTTTTCACTCTATTTCACTCT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
       AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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Pred. No. 1.7e-161;
0; Mismatches 37;
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/organism="Homo sapiens"
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Embryogenesis associated proteins
Patent: WO 0248362-A 4 20-JUN-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Retroviral nucleic material and nucleotide fragments, in particular, associated with multiple sclerosis and/or rheumatoid matchritis, for diagnostic, prophylactic and therapeutic uses Patent: JPP 2002509437-A 9 26-MAR-2002;
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07-JUL-1997 FR 97/08816
GLAUCIA PARAHNOS BACCALA FLORENCE KOMURIAN PRADEL, FREDERIC
        12531 CACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATTATTGCCT
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Retroviral nucleic material and nucleotide fragments,
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CC associated with multiple sclerosis and/or
rheumatoid arthritis,
CC diagnonia.
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                                                                                                                                                                                                                                                                                                  12351 TATTAAATCTTGCAACTTCAAAAAAGAAAAAGATA 12316
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Strandedness: Single;
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85.8%; Score 545; DB 6; 1

Best Local Similarity 92.4%; Pred. No. 4.3e-161;

Matches 572; Conservative 0; Mismatches 47;
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/mol_type="genomic DNA"
/db xref="taxon:32644"
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BD136199
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Genoscope / Centre National de Sequencage
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Location/Qualifiers
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Pred. No. 4.8e-161;
0; Mismatches 40;
                                                                                  The following BAC sequence is oriented
                                Web site: http://www.genoscope.cns.fr/
Contact: SegRef@genoscope.cns.fr
                                                                                                                 Assembly program: Phrap; version 2.0 Quality coverage: 8.21x in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="matching EMBL: Z52518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="matching EMBL: T77897
                                                                                                   ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-11"
136833. .137011
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Range : bases
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93.2%;
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1 (bases 1 to 1329)
Ott, C. and Bedin,F.
RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR
RECROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR
ASSOCIATED WITH MULTIPLE SCHEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR
DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES
PALENT: WO 9902666A 12 21-JAN-1999;
BIO MERIEUX (FR); OTT CATHERINE (FR)
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GCATCCATCTTTAAACATGGGGCTTGCAACTTAGCTCACACCGACCAATCAGAGGGCTC
                                                                                                                                                                                                                                                                                                                                                                          AGAGCACAGGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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                                                                                                177 CIGGACCGGCCIGCTAGACTAIGCFCTGAFGTTAATGACATTGAAGTCACCCCTCCCGAG
                                                                                                                                                                                                                               AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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                                     CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                                                                                                   GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                                                                                                                   GAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGGAAGCAGTTAGAGCAGT
                                                                                                                                                                                 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
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Pred. No. 4.3e-161;
0; Mismatches 47;
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Best Local Similarity 92.4%;
Matches 572; Conservative
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                                                                                                                           CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                       caaatagtrictricaaatggaaccccagargcagtccargactaaaarcracgragaccc
                                                                                                                CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                              GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                                                                                                                                           AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                                                                                                                                                                                          GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGGTC
                                                                                                                                                                                                                                                                                                                                                        ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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Perron, H., Beseme, F., Bedin, F., Paranhos-Baccala, G.,
Komurian-Pradel, F., Jolivet-Reynaud, C. and Mandrand, B.
Isolated nucleotide sequences associated with multiple
rheumatoid arthritis and a process of detecting
Patent: 15,82703-A 108 24-JUN-2003;
Location/Qualifiers
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Pred. No. 4.3e-161;
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Sequence 108 from patent US 6582703.
AR344389.1 GI:33740310
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTANATCTTGCAACTGAA 619
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ilarity 92.4%;
Conservative
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Unclassified.
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Best Local Similarity
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Aav43215 Multiple
Aax29702 Clone CL6
Adg14843 MSRV asso
Adb84397 MSRV-1 as
Aaa63826 Nucleotid
Aa46125 Human EMB
Aav43219 Multiple
Aax29704 Clone 5M6
Adg14849 MSRV asso
Acc14454 Human gen
Acc4677 Human gen
Acc4677 Human dit
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                                                                     February 21, 2005, 06:25:25; Search time 327.546 Seconds (without alignments) 11476.370 Million cell updates/sec
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	21	522.	۰-	82.3	2782	0	AAX25661	
	22	522.6	·	82.3	2782	m	AAA59211	Aaa59211 5' non co
	23	522.6	·-	82.3	2782	ß	AAH20069	Aah20069 HERV-W en
	24	517.4		81.5	2930	v	AAD24195	Aad24195 Human syn
	25	516.2		81.3	56093	9	ABL61744	Abl61744 Colon ade
	26	511.4		80.5	7582	7	AAX25665	Aax25665 Complete
	27	511.		80.5		m	AAA59215	Aaa59215 Human end
	28	510.		80.4	4	٣	ABN97978	Abn97978 Human ret
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	30	505.8		79.7	10499	m	ABN97929	Abn97929 Human ret
	31	500.8		78.9	285020	1	ACN44958	Acn44958 Human gen
	32	499.6		78.7	1894	4	AA114608	Aai14608 Probe #45
	33	499.6		78.7		4	ABA56337	Human
	34	499		78.7		4	AAI35980	Probe
	35	499.6		78.7	1894	4	ABA45822	Human
	36	499		78.7		4	ABA25978	Aba25978 Probe #44
	37	499.		78.7		4	AAK30018	Aak30018 Human bon
	38	499.		78.7		4	AAK04516	Aak04516 Human bra
	39	499.		78.7		4	ABS29670	Abs29670 Human liv
	40	499.		78.7	1894	ហ	AAI04422	Aai04422 Probe #44
	41	499		78.7		9	ABS04589	Abs04589 Human gen
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	43	495.		78.0		~	AAX25663	
	44	495.	9	78.0		ო	AAA59213	Aaa59213 Partial p
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## ALIGNMENTS

AAV43215 standard; cDNA; 635 BP

RESULT 1

AAV43215

AAV43215;

New nucleic acid from retroviruses - useful for diagnosis, prevention and treatment of, e.g. multiple sclerosis. Multiple sclerosis associated retrovirus; MSRV; MS; pol gene; gag gene; env gene; rheumatoid arthritis-associated virus; ss. /\*tag= a /product= "Encodes protein AAW71067" Multiple sclerosis associated retrovirus fragment 4. Perron H, Beseme F, Bedin F, Paranhos-Baccala Komurian-Pradel F, Jolivet-Reynaud C, Mandrand Multiple sclerosis associated retrovirus Disclosure; Page 183; 286pp; English. Location/Qualifiers 1. .234 96US-00756429. 97WO-IB001482 (first entry) WPI; 1998-322732/28. P-PSDB; AAW71067. (INMR ) BIO MERIEUX WO9823755-A1 26-NOV-1997; 29-DEC-1998 26-NOV-1996; 04-JUN-1998. 

The present sequence represents a multiple sclerosis (MS) associated retrovirus (MSRV) genomic fragment used in the method of the invention.

Adc38776 Human cDN Abk89296 Human gen Aqg94981 Human kin Aaf5530 Nucleotid Aax25660 Human end Aax25660 Human end Aaa59210 3' pol ge

AAF55630 AAX25660 AAA59210

ADQ94981 **ABK89296** 

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The invention provides complete or partial genomic sequences of the MSRV-1 pol gene, gag gene and env gene, and polypeptides encoded by these genes. The invention also provides antibodies raised against the polypeptides. The genomic sequences, polypeptides and antibodies are also claimed useful for diagnosing infection by MS and rheumatoid arthritis-associated viruses, and also for prevention and treatment of infection with these viruses
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                                                                                              This sequence represents clone CL6-3' from a novel multiple sclerosis related virus type 1 (MSRV1). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis. (Updated on 27-ANG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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Nucleic acid sequences of retrovirus called MSRV-1 - associated with
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                                                                                                                                                                                                                                                  Sequence 635 BP; 188 A; 170 C; 136 G; 141 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                   100.0%; Score 635; DB 2;
ilarity 100.0%; Pred. No. 1e-186;
Conservative 0; Mismatches 0.
                          multiple sclerosis or rheumatoid polyarthritis
                                                                   Page 36-37; 83pp; French
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New isolated or purified nucleic acid associated with multiple sclerosis and/or rheumatoid arthritis, useful for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample.
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Jolivet-Reynaud C, Mandrand
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KOMURIAN-PRADEL F.
JOLIVET-REYNAUD C.
MANDRAND B.
GARSON J A.
TUKE P W.
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BESEME F.
BEDIN F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid which comprises the gene of a retrovirus associated with multiple sclerosis or rheumatoid arthritis. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Garson JA,
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                                   ; Pred. No. 1e-186; 0; Mismatches 0
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                                                                                                                                                                                                                                                      Multiple sclerosis associated retrovirus.
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Best Local Similarity 100.0%;
Matches 635; Conservative 0
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cc multiple sclerosis-associated virus (MSRV)-1. The nucleic acids comprise proteins or defined peptides (including immunodominant peptides) encoding the proteins or defined peptides (including immunodominant peptides) antigenic peptides or conserved mocife). Also included are a process for detecting a virus associated with multiple sclerosis or rheumatoid or arthritis in a biological sample, a nucleic acid probe for the detection of a virus associated with multiple sclerosis or rheumatoid arthritis, a primer for the amplification by polymerisation of a nucleic acid of a virus associated with multiple sclerosis or rheumatoid arthritis, a polypeptide exhibiting an inhibitory activity on the proteolytic, reverse transcriptase or ribonuclease H activity from MSRV, and an antibody directed against the MSRV-1 virus obtained by immunogenic agent consisting of the antigenic polypeptide defined above. The nucleic acids are useful for detecting a biological sample a virus associated with multiple sclerosis or rheumatoid arthritis, or for detecting in a biological sample, the presence of or exposure to a virus associated with multiple sclerosis or rheumatoid arthritis, or for sequence is a claimed MSRV-associated equence whose identity cannot be accurately determined. Note: The SRQ ID numbers for the sequences as displayed in the main body of the patent do not match the SRO ID numbers or in the sequence listing. Consequently those sequences mentioned in the numbers intended to claim.
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Pred. No. 6.4e-184;
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Local Similarity 98.6%;
les 626; Conservative
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The present sequence represents the nucleotide sequence corresponding to the 3' env region and long terminal repeat sequences from clone CL6 of Multiple Sclerosis retrovirus (MSKV-1). The specification describes a long terminal repeat (LTR)-RUS region which encodes the expression of a MSKV-1 protein. This is unusual for LTRs, in particular in the RUS region. The sequence includes CAAT and TATA signals which are present in the US and are not directed towards the CDS indicated in the features table. Probes and antibodies to the MSKV-1 retrovirus presence of MSKV-1 retrovirus in a biological sample. (Updated on 06-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAACTGTAAAACTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide fragment of LTR-RUS region from Multiple Sclerosis retrovirus (MSRV) used to detect the presence of MSRV-1 retrovirus in a biological
                                                                                                                     MSRV-1; pol region; long terminal repeat; LTR; RU5 region; retrovirus;
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                                                                                              Nucleotide sequence of the MSRV-1 3' env and LTR regions.
                                                                                                                                                                                   Location/Qualifiers
1. .1629
/*tag= a
/note= "Contains one termination codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Komurian-Pradel
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                                                                                                                                                                Multiple sclerosis associated retrovirus.
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         BP.
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Best Local Similarity 98.3%;
Matches 624; Conservative
         AAA63826 standard; DNA; 2030
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/*tag=
1800. .1
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1858. .;
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04-DEC-2000
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AAA63826
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and nucleic acid molecules encoding such proteins. EMBRY sequences are useful for screening modulators useful for treating or preventing disorders associated with abnormal expression of EMBRY. The disorders are include reproductive disorders such as infertility, endometriosis, endometrial or ovarian tumour; autoimmune/inflammatory disorder such as acquired immune deficiency syndrome (AIDS), allergies, contact dermatitis; disorders of the placenta such as precelampsia, abruptio placentae etc. Sequences of the invention are also useful for analysing a proteome of a tissue or a cell type. EMBRY proteins are useful as immunogens for preparing antibodies. Polynucleotides of the invention are useful for creating knockin humaniaed animals or transgenic animals to model human diseases. They are also used in gene therapy. The
                                                                                                                                                                                      New polypeptides of human embryogenesis associated proteins for screening modulators useful for treating or preventing disorders e.g. endometriosis, infertility, allergy, preeclampsia.
                                                                                                                                                                                                                                                                         invention relates to human embryogenesis associated proteins (EMBRY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTAATGACATTGAAGGCACCCCTCCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2074 BP; 583 A; 567 C; 392 G; 531 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence is human EMBRY-2 cDNA
                                                                                                                                                                                                                                               Claim 59; Page 96-97; 97pp; English.
                                      14-NOV-2001; 2001WO-US043956
                                                                15-NOV-2000; 2000US-0249407P
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llarity 93.8%;
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Best Local Similarity
Matches 579; Conserv
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CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGACTGAGAGAC
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                                                                                              CTGGACCGGCCTGCTAGCCCCATGCTCCGATGATGACATTGAAGGCACCCTCCCGAG
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                                         CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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product= "Mature EMBRY-2 protein"
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/*tag= b
124. .1689
/*tag= c
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Multiple sclerosis; virus; diagnosis; prophylaxis; therapy; expression;
rheumatoid polyarthritis; ss.
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                                                                                                                CTGGACCGGCCTGCTAGCCCATGCTCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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                                                  cecretaterreaacrrecrretraagrrigrererreagaarreaagergraagera
                                                                                   GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
Pred. No. 1.5e-158;
0; Mismatches 47;
                                1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCT
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  92.48;
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   Best Local Similarity 92.4
Matches 572; Conservative
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27-AUG-2003
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                  nucleic acid from retroviruses - useful for diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                         a stop
                                                                                                                                                                                                                                                                                                                                                                                             for a stop
                                                                                                                                                                                                                                                    Liple sclerosis associated retrovirus; MSRV; MS; pol gene; gag gene; gene; rheumatoid arthritis-associated virus; ss.
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
2. .490
/*tag= a
/product= "Encodes protein AAW71069"
/trans_except= (pos:77-79, appears to code for a stop
      AGAGCACAGGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                       (pos:125-127, appears to code for
                                                                                                                                                                                                                                                                                                                                                                                              code
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/transl_except= (pos:137-139, appears to codon)
                                                                                                                                                                                                                                   Multiple sclerosis associated retrovirus fragment 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bedin F, Paranhos-Baccala
Jolivet-Reynaud C, Mandrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 187-188; 286pp; English.
                                                                                                                                                                                                                                                                                       Multiple sclerosis associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of, e.g. multiple sclerosis.
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                                                                                                                                                                      AAV43219 standard; cDNA; 1329
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                                                                                             ATTAAATCTTGCAACTG
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Length 1329;

Score 545; DB 2;

85.8%;

Query Match

540

420 919 480 736

240

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300 556 360 919 196 900

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New isolated nucleic acid and their fragments having the pol gene of a retrovitus, useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid which comprises the gene of a retrovirus associated with multiple sclerosis or rheumatoid arthitis. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthitis. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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                                                                          rheumatoid arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
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Jolivet-Reynaud C, Mandrand
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Pred. No. 1.5e-158;
0; Mismatches 47;
                                                                           gene; retrovirus; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 108; 193pp; English
                                                                                                          Multiple sclerosis associated retrovirus
                                                                                                                                                                                                            03-APR-2002; 2002US-00114104
                                                                                                                                                                                                                                           96US-00756429
97US-00979847
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Best Local Similarity 92.4%;
Matches 572; Conservative
             entry)
                                                                                                                                                                                                                                                                                                                           124
                                            MSRV associated cDNA
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Komurian-Pradel F,
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                                                                                                                                                              This sequence represents clone 5M6 from a novel multiple sclerosis related virus type 1 (MSRV1). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritus. (Updated on 27-ANG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aggactracciggatiticctraggctgactragaatcccnaagcctanctgggaaggtgacc
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                                                                                - associated with
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                                                                               acid sequences of retrovirus called MSRV-1 sclerosis or rheumatoid polyarthritis.
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                                                                                                                                                                                                                                                                                                                Score 545; DB 2; I
Pred. No. 1.5e-158;
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                                                                                                                                 Claim 1; Page 39-40; 83pp; French
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ilarity 92.4%;
Conservative
                                  WPI; 1999-098275/09.
P-PSDB; AAW99554.
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Best Local Similarity
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              CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
                                                                                                                                                                                               AGAGCACAGCGGGAGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
                                                                                        CTGGACCGGCCTGCTAGCCCCATGCTCGATGACACTTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                             CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGA
                                                                                                                                                                                                                                                                                                                       AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGAAGGTGACT
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17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-0299428P.
20-JUN-2001; 2001US-0299776P.
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29-MAR-2001; 2001US-0280067P.
29-MAR-2001; 2001US-0280068P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening drug candidates; (ii) for screening of bioactive agent capable of bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vi) for tasating carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma are apprehensively to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding capacinome. This patent is an equivalent to basic patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19571 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATTGAAACTGTAAAACTA 19630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                          Agagcacadegggaaggacaaggatreggarataaactcaggcatrcaagcaagagaacag
                                                                                                                                                          AGAGCACAGGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                    CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21646 BP; 5145 A; 5617 C; 5218 G; 5646 T; 0 U; 20 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 21646;
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94.8%; Pred. No. 1.8e
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 910; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genomic sequence hCG1748307
                                                                                                                                                                                                                 601 ATTAAATCTTGCAACTGAA 619
                                                                                                                                                                                                                                       ATTAAATCATGCAACTGCA 875
                                                                                                                                                                                                                                                                                                                                                    ACN44454 standard; DNA; 21646
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les 562; Conserv
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Matches
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ACN44454
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1051 AGAGCACAGGAGGGAGGACAAGGATCGGGATATAAACCCGGGCATTCAAGCCGGCAATGG 1110
                                                                                                                                                                                                                                                                      The invention relates to an isolated or purified nucleic acid from a virus associated with multiple sclerosis and/or rheumatoid arthritis, unltiple sclerosis associated virus (MSRV)-1. The nucleic acids comprise pol, gag or reverse transcriptase genes (or their fragments) encoding the proteins or defined peptides (including immunodominant peptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated or purified nucleic acid associated with multiple sclerosis and/or rheumatoid arthritis, useful for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample.
                                                                                                                                                     GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                                                   421 ACTABABATGCTBATTAGGCAABAATAGGAGGTAAAGBAATAGCCAATCATCTATTGCCTG
                                                                                                                                                                                                                                                                                                                                  AGAGCACAGCGGGACGACGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
                                                                     AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                          CAACCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                               1111 CAACCCCCTTTGGGTCCCCTTCCTTTGTATGGGAGCTCTGTTTTCACTCTATT
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Jolivet-Reynaud C, Mandrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSRV-1 associated DNA sequence #21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 31; Page 80; 193pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOMURIAN-PRADEL F.
JOLIVET-REYNAUD C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-512253/48
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GARSON J A.
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BESEME F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUKE P W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified;.
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(MAND/)
(GARS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TUKE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel human diagnostic and therapeutic Dolymucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates to polymucleotide sequences at least 90% identical to the dithp CDNA sequences of the invention; recombinant vectors, host cells and sequences of the invention; recombinant vectors, host cells and transgenic organisms comprising a dithp nucleic acid sequences; methods of proteins microarrays comprising dithp nucleic acid sequences; methods of detecting dithp nucleotide and protein sequences; methods of corpobe. Dithp nucleic acid sequences and DITHP proteins and methods of assessing the toxicity of test compounds using a dithp hybridisation probe. Dithp nucleic acid sequences and DITHP proteins may be used in the assessing the toxicity of fconditions including cancer and other cell conditions including cancer and other cell proliferative disorders; autoimmune or inflammatory disorders; bacterial, viral, fungal or parasitic infections; hormonal disorders; metabolic disorders; neurological disorders; gastrointestinal disorders; transport disorders; and connective tissue disorders. They may also be used to screen for modulators of protein acityty or gene expression. DITHP proteins can additionally be used in analysis of the proteome of a tissue or cell type and to induce antibodies. They may also be used to additionally useful in somatic or germline gene therapy of the disorders and additionally useful in somatic or germline gene therapy of the disorders or cell type and to induce antibodies. They may also be used to the protein additionally useful in somatic or germline gene therapy of the disorders and primers, in genotyping and identification of individuals, in the generation of transgenic animal models of human disease or knock in the generation of transgenic animal models of human disease or knock in which is pastent dimet form part of the printed specification, which is patent directions of the protein acids a
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                                                                                                                                                                                                                                                                                              Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynuclectide, and to induce antibodies.
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                                                                                                                                          Kleefeld Y, Gerstin EH;
Panzer SR, Harris B;
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                                                                                                   Chinn J;
Amshey SR;
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                                                                                                   Gietzen D,
O, Yap PE,
                                                                                                                                                                                        Urashka ME;
                                                                                                Daffo A, Jones AL, Tran AB, Dahl CR, Giet Dufour GE, Hillman JL, Yu JY, Tuason O, Y Daughtery SC, Dam TC, Liu TF, Nguyen DA, Page CH, David MH, Lewis SA, Chen AJ, Flores V, Marwaha R, Lo A, Lan RY, Urashly
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                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; SEQ ID NO 668; 591pp; English.
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                20-JUN-2001; 2001US-0300001P
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                                                           (INCY-) INCYTE GENOMICS INC.
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                                                                                                                                                                        Peralta CH, David MH,
Flores V, Marwaha R,
                                                                                                                                                                                                                                      WPI; 2003-129518/12.
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AAX77526;

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antigenic peptides or conserved motifs). Also included are a process for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample, a nucleic acid probe for the detection of a virus associated with multiple sclerosis or rheumatoid arthritis, a primer for the amplification by polymerisation of a nucleic acid of a virus associated with multiple sclerosis or rheumatoid arthritis, a polymeristation of a nucleic acid of a virus that a polymeristation an inhibitory activity on the proteolytic, reverse transcriptase or ribonuclease H activity from MSRV, and an antibody directed against the MSRV-1 virus obtained by an antibody activity a human or animal body or cells with an immunogenic agent consisting of the antigenic polypeptide defined above. The nucleic acids are useful for detecting a biological sample a virus associated with multiple sclerosis or rheumatoid arthritis, or for detecting in a biological sample, the presence of or exposure to a virus associated with multiple sclerosis or rheumatoid arthritis. The present sequence is a claimed MSRV-associated sequence whose identity cannot be accurately determined. Note: The SEQ ID numbers for the sequences as a displayed in the main body of the patent do not match the SEQ ID numbers in the sequence listing. Consequence whose sequences mentioned in the claims may not be the sequences the authors intended to claim.
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Sequence 1329 BP; 339 A; 346 C; 282 G; 332 T; 0 U; 30 Other;

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Score 535; DB 9; Length 1329;
Pred. No. 1.9e-155;
0; Mismatches 57; Indels
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This invention describes novel human secreted proteins encoded by polynucleotides isolated from human adult testes, adult brain, adult blood or adult placenta, or murine adult bone marrow or thymus cDNA blood or adult placenta, or murine adult bone marrow or thymus cDNA activities which would make them unitable for treating, preventing or activities which would make them unitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional continity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemostatic activity, and thrombolytic activity, chemotactic/emoximineic activity, haemostatic activity, and thrombolytic activity, receptor/ligand activity, and tumour activity, and tumour activity, adherin/tumour invasion suppressor activity, and tumour furnition activity. The polynucleotides are also stated to be useful for
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                                                                                                                                                 Secreted protein; testes; brain; blood; placenta; human; murine; thymus; bone marrow; treatment; prevention; nutrition; cytokine; immune; vaccine; cell proliferation; cell differentiation; suppressor; tumour inhibition; haematopoiesis regulator; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; tumour; cadherin; tumour invasion suppressor; gene therapy; tissue growth; ss.
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                                                                                                                     Human secreted protein AJ172_2 cDNA.
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This is the human secreted protein AJ172 2 nucleotide sequence, obtained from a human adult testes CDNA library. The invention relates to secreted human and murine proteins. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or amelorating medical conditions in humans and animals. Detection of the levels of the proteins can be used for the clasmosis of e.g. pre-eclampsia, placental pathology or cancer. Agents which modulate the expression or function of the proteins may be used for treating a neoplastic disease and inhibiting metastasis. Other suggested activities include nutritional activity (e.g. in feeds). Cytokine and cativities include nutritional activity, immune stimulating (e.g. as cacivities) or suppressing activity, haemostatic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, creeptor/ligand activity, and tumour inhibition activity. The invasion suppressor activity, and tumour inhibition activity. The polynucleotide sequences are also stated to be useful for gene therapy
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Pred. No. 6.6e-155;
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                                                                                                                     AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                                                                                     AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTAGGTGGGAAGGTGACC
                                                                                                                                                                                                                                                                                        2671 ACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTGACCAATCAGAGGGCTC
                                                                                                                                                                                                                                                                                                                                                                              2731 ACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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                                               GAAATCTCAGCTGCACACACCTCTACTACGCCCCAATTCAGCAGAAGCAGTTAGAGCGGT
                                                                                                CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGCTTGAGAGAC
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                                                                                                                                                                                                                                                           GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGACCAATCAGAGAGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ59468 standard; cDNA; 2946
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98US-00175928
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20-OCT-1998;
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US2002193567-A1.
                                                 Homo sapiens
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Merberg D,
Kelleher K;
                                                                                                        25-OCT-1996
30-OCT-1996
        18-DEC-2003
                                                                               07-JUN-1996
                                                                                                  27-SEP-1996
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10-APR-1997
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                                                            19-DEC-2002
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                                                                                                                      05-SEP-1997
  ADC38776;
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CAACCCCTTTGGGTCCCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT 600
                response syndrome (SIRS), ischaemia-reperfusion injury, Crohn's disease, anaphylaxis and hypersensitivity. Proteins are also useful for inducing tumour immunity, for inducing bone, cartilage, tendon, ligament and/or nerve growth or regeneration, for proliferating neural cells and for regenerating nerve and brain tissue, for inducing fertility and for inhibiting tumour growth. Proteins are also useful as chemokine for mammalian cells (e.g., monocytes, fibroblasts, neutrophils), and also useful as inhibitors of receptor/ligand interactions. The present
coagulation disorders, inflammatory diseases (e.g. systemic inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CTGGACCGGCCTGCTAGCCCCATGCTCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                                                                                                                                                                                                 DB 10; Length 2946;
                                                                                                                                                                                                                                                  Sequence 2946 BP; 858 A; 801 C; 570 G; 717 T; 0 U; 0 Other;
                                                                                                                                                                                                       sequence represents cDNA encoding a human secreted protein.
                                                                                                                                                                                                                                                                                                                                           42; Indels
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Pred. No. 6.6e-155;
0; Mismatches 42;
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91.5%;
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Matches 581; Conservative
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                                                                                                                                                                                       autolmmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; allergic reaction; asthma; myeloid cell deficiency; pymphoid cell deficiency; prepoporosis; osteoarthritis; peripheral nervous system disease; peripheral neuropathy; Alzheimer's disease; Parkinson's disease; coagulation disorder; inflammatory disease; systemic inflammatory response syndrome; SIRS; ischaemia-reperfusion injury; Crohn's disease; anaphylaxis; hypersensitivity; regeneration; neural cell proliferation; fertility; tumour; chemokine; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins AZ3021 encoded by clone AZ3021 from human adult colon, and BD12716 encoded by clone BD12716 from human fetal kidney cDNA library, useful for treating e.g. multiple sclerosis and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Σ
                                                                                                                                                                      severe combined immunodeficiency; SCID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collins-Racie LA, Evans C;
Spaulding V, Carlin-Duckett
                                                                                                                              Human cDNA encoding a secreted protein #63.
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96US-00628314.
96US-00659231.
96US-00664596.
96US-0067231.
96US-00701819.
96US-00701819.
96US-00721488.
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96US-00739775.
97US-00833823.
97US-00837677.
97US-00924838.
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                                                                                                                                                                         gene; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEMY ) GENETICS INST INC.
                                                                                    (first entry)
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P-PSDB; ADC38777.
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420

2610

300

2430

9

Gaps

12;

2490

240

180

2790

480

540

635

Human; ds; gene; serine/threonine protein kinase; inflammation; cancer;

Human gene for novel serine/threonine serine kinase.

<pre>/*tag= bb /standard_name= "Single nucleotide polymorphism" replace(31808,T) /*tag= br</pre>	e a	/*tag= bd /standard_name= "Single nucleotide polymorphism" replace [34511,G)	<pre>/*tag= be /standard name= "Single nucleotide polymorphism" replace (3518,G) /************************************</pre>	/_cag=/ /standard name= "Single nucleotide polymorphism" replace[35463,C] /*tag= bg	/standard_name= "Single nucleotide polymorphism" replace(35477,T) /*tag= bh	/Brandard hamme= "sligle nucleotide polymorphism replace(37050,G) /*tag= bi	ard name= "Single e(37470,G) bj	/standard_name= "Single nucleotide polymorphism" replace(17481,A) /*taq= bk	/standard_name= "Single nucleotide polymorphism"   replace(37499,T)   replace(37499,T)	H (	/*tag= bm /standard name= "Single nucleotide polymorphism" renlace(40787.A)	<pre>/*tag= bn /*tag= bn /standard_name= "Single nucleotide polymorphism"</pre>	replace(44582,G) /ttag= No /crands homes "Single muslectide polymorphism"		<pre>ird name= "Single nucleotide s(46091,T) bq</pre>	H 0	e a	E 0	/res= "free   Single nucleotide polymorphism"   replace   50802,T   replace   50802,T	/rest in name= "Single nucleotide polymorphism" replace(53305,A)	/rtag= bv /standard name= "Single nucleotide polymorphism" replace(5337853380,GG)	/*teg= bw /fatandard name= "Single nucleotide polymorphism" 53738. 5 <u>5</u> 903	/*tag= d /number= 2	5390483114 /*tag=	ഥവ
variation	variation	variation	variation	variation	variation	variation	variation	variation	variation	variation	wariation		variation	variation	variation	variation	variation	variation	variation	variation	variation	exon		intron	variation
	Homo sapiens. Key Location/Quali	variation	variation replace(1399,G /*tag= aj /standard_name	FT variation replace(18711873,TG) FT /*tag= ak FT /feadard name= "Single nucleotide polymorphism" reproduce(1877,TA)	/*tag= al /standard nam CDS 3000323016	FT /*tag= a /*tag= b // Prag= a // Prag= a // Prag= // Pr				PT variation replace(7590,A) FT /*tag= an /*tag= n //tag= n /single nucleotide polymorphism"	variation replace(9315,C) /*tag= ao /*tag= ao /*tag= ao /*tag= ao	<pre>/Brandard hame= 'Single nucleotide po variation replace(9572,A) /*tag= ap /*tag= ap</pre>	/standar variation replace	/*tag= aq FT /*tandard_name= "Single nucleotide polymorphism" FT variation replace(1137911380,AAA)	/*tag= ar /standard_name= renlace(12478_A		variation replace(12486. /*tag= at /standard_name=	بعو. معور	variation replace(25444. /*tag= av /standard_name=	variation		variation replace(28107,Y) /*taga ay /*taga ay	/brailarion registration representation replace(28178,R) /*tags as	/ cay- /standar variation replace(	FT /*tag= ba   standard_name= "Single nucleotide polymorphism"   FT variation replace(29535,G)

	1/0462 GUILLTACCIIIAAACCCGGGGGCAAAAAIAGGGGGAAAGAAAAAAAA			Db 170282 dagdaatdaggraccartriftgggreccereccertrigratggggerergriftgggreger 170223	170222	RESULT 17 ADQ94981/C TT REGION OF STAND 326014 RP	ADQ94981;			Annass; aragnosts, career, crees strong and argay; cytostatic; gene the single nucleotide polymorphism; gene; de.	Homo sapiens.	Key variation	FT /*Landard name= "Single nucleotide polymorphism (SNP)" FT variation replace(1399,G)	variation	variation	name= 3016	~~~	FT exon 30003169 FT /*tag= e FT intron 317053737	variation regard (3180,A)	/standard_name= "Single nucleotide polymorphism (SNP) variation replace(7590,A) *tad= i /*tad= i /*tad= i	<pre>/standard name= "Single nucleotide polymorphism variation replace(9315,C) /*tag= j</pre>	dard_name= "Single nucleotide polymorphism ce(9572,A)	
<pre>/standard name= "Single nucleotide polymorphism" variation replace(56453,C) /*tag= by</pre>	<pre>/standard_name= "Single nucleotide polymorphism" variation replace(59300,T) /*tag= bz /standard_name= "Single nucleotide polymorphism"</pre>	replace (60998, A) /*tag= ca /standard name=	<pre>variation tepiace(v3213,7.7) /*tag= cb /standard_name= "Single nucleotide polymorphism" variation replace(63293,A)</pre>	/*tag= cc /*tag= cr /*tag= variation replace(64181,T)	/*tag= cd /gtandard_name= "Single nucleotide polymorphism" variationreplace(64191,A)	<pre>/*tag= ce /standard_name= "Single nucleotide polymorphism" variation replace(68992,C) /*tag= cf</pre>	/gtandard_name= "Single_nucleotide_polymorphism" variation replace(75246,Y)	<pre>/standard_name= "Single nucleotide polymorphism" variation replace(77368,G) /*tag= ch</pre>	/standard_name= "Single nucleotide polymorphism" variation replace(70043,A)	/*tag= ci /standard_name= "Single nucleotide polymorphism" variation replace(79195,T)		Variation reprace (x - x - x - x - x - x - x - x - x - x	"Single micleotide	variation replace(81065,C) /*tag= cm /*tag= cm	Query Match  83.9%; Score 532.8; DB 6; Length 326014;  Best Local Similarity 90.5%; Pred. No. 1.3e-153;  Matches 583; Conservative 0; Mismatches 52; Indels 9; Gaps 1;	FTAACCTCC		CTGGACCGGCCTGCTAGCCCATGCTCGATGTTAATGACATTGAAGGCACCCCTCCCGAG		181 GAAATCTCAACACACACCCCTACLAACCCCCAATTCAGGGAAGGAAGTAGAGGGT 170583	241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGACTGAGAGAC 300	360	170522 AGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT 170463

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/*tag= aj /standard_name= "Single nucleotide polymorphism (SNP)" replace(44582,G) /*tag= ak /standard name= "Single nucleotide polymorphism (SNP)"	nucleotide polymorphism	replace(46091,T) /*tag= am /*tag= am /*fandard name= "Single nucleotide polymorphism (SNP)" replace(47084,C)	/*tag= an //standard_name= "Single nucleotide polymorphism (SNP)" replace(48013.T) /*tag= // *tag= "sizalo nucleotide polymorphism (SNP)"	"Single nucleotide polymorphism	nucleotide	replace(53305,A) /*tag= ar /standard_name= "Single_nucleotide_polymorphism (SNP)"		5373853903 /*tag= at 5390483114		ard_name= "Single nucleotide polymorphism (SNP) e(\$5453,C) aw	/standard_name= "Single nucleotide polymorphism (SNP)" replace(59300,T) /************************************	ird name= "Single nucleotide polymorphism (SNP) 2(60998,A)	ordiname= "Single nucleotide polymorphism (SNP) (63013,A) az	<pre>ird_name= "Single nucleotide polymorphism (SNP) s(63293,A) ba</pre>	8 0	/_cay=/ /standard_name= "Single nucleotide polymorphism (SNP)" replace(64191,A) /*tag= hc	/standard_name= "Single nucleotide polymorphism (SNP)" replace(68992.C) /*tag= hd	<b>2</b> 0	/eradard_name= "Single nucleotide polymorphism (SNP)" replace(77368,G) /**:	H (	/_rag= 29 /standard_name= "Single nucleotide polymorphism (SNP)" replace(79395,T) /*toc bh	//cag= //standard name= "Single nucleotide polymorphism (SNP)" replace(79474,G)
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The present sequence encodes a human endogenous retrovirus envelope protein. The specification describes a method for detecting expression of an envelope protein from a human endogenous retrovirus (HERV), in cells, of a tissue or culture. The method comprises detecting syncytia formation due to the fusogenic properties of the envelope protein. Envelope polypeptides and polymucleotides are used to produce therapeutic or prophylactic compositions, particularly for treatment of cancer, to correct defects in placental development (or other natural formation of other types of syncytia), and to promote adhesion of cells in grafts or cellular repair processes. Expression of sequences antisense to the polymucleotide are used to prevent formation of syncytia
                                                                                                                                                                                                                                                         Detecting expression of human endogenous retrovirus envelope protein in cells of a tissue or culture, from its ability to induce syncytia.
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Pred. No. 2e-154;
0; Mismatches 43; Indels 12;
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                                                                                                                                                                                          Bouton O,
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/product= "envelope protein"
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(INRM ) INST NAT SANTE & RECH MEDICALE.
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91.3%;
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99FR-00011793.
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Matches 580; Conservative
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                                                                                                                                                                                                CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGGGGACCC
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syncytia; cancer; cell adhesion; ss.
                                                                                      Length 326014;
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                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Autoimmune disease; retrovirus; human endogenous retrovirus W; HERV-W; gag gene; pregnancy; multiple sclerosis; T cell proliferation; ss.
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                                                                                                               CATCAGCCAACTCCCCCAACAGCACTTGGGTTTTTCCTTGAGAGGGGGGACTGAGAGAC
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CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pol gene and 3' non coding sequences of HERV-W from human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTANATCTTGCAACTGAAAAAAAAAAAAAAAA 635
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Pred. No. 1.3e-152;
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 fragment, which is associated with an autoimmune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell
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Pred. No. 1.3e-152;
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Clone; human endogenous retrovirus; genome; autoimmune disease;

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polyarthritis; insulin-dependent diabetes;
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         multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diak
disseminated lupus erythematosus; pregnancy; chromosomal marker; ss
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Pred. No. 2e-151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.3%;
90.4%;
                                                                                                                                                                                                                         98WO-FR001442
                                                                                                                                                                                                                                                                       97FR-00008815
                                                                                  endogenous retrovirus
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                                                                                                                                                                                                                                                                                                                                                                    Blond J,
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-120897/10.
                                                                                                                                                                                                                                                                                                                   (INMR ) BIO MERIEUX
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                                                                                                                                                                                                                                   2386 GGTCGGCCAACCTCCCCAACAGACTTAGGTTTTCCTGTTGAGATGGGGGGACTGAGAGA
                                                                                                                                                                                                                                                                                                                                   2446 AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCTTAAGCCTAGGTGGGAAGGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAACCCCTTTGGTCCCCTCCCTTTGTATGGCGCTCTGTTTTCACTCTATTTCACTCT
                                                                                                                            AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGAAGGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                             2506 ACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCGACCAATCAGAGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2566 ACTADADATGCTAATTAGGCAAAGACAGGAGGTAAAGAAATAGCCAATCATTATTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human endogenous retrovirus; HERV-W; HERV; chromosome 7; env protein; envelope protein; multiple sclerosis-related superantigen; vaccine; surface antigen; transmembrane; multiple sclerosis; neuroprotective; antisense-therapy; autoimmune disorder; ds.
                            361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
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CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                               241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
                                                                                               181 GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V-W envelope protein G"

(pos:792. .792.aa:Phe)

(pos:812. .795,aa:Thr)

(pos:812. .814,aa:Leu)

(pos:818. .820,aa:Ser)

(pos:865. .864,aa:Tyr)

(pos:865. .864,aa:Tyr)

(pos:1174. .1176,aa:Tyr)

(pos:1174. .1176,aa:Arg)

(pos:1174. .1176,aa:Arg)

(pos:2017. .2019,aa:Lu)

(pos:2017. .2019,aa:Lys)

(pos:2044. .2046,aa:Arg)
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/transl_except=
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5'UTR
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                                 2685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid from human endogenous retrovirus, useful e.g. for diagnosis of autoimmune disease and complications of pregnancy, contains at least part of the gag gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Autoimmune disease; retrovirus; human endogenous retrovirus W; HERV-W; gag gene; pregnancy; multiple sclerosis; T cell proliferation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAACTGTAAAACTA
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  2686 CAACCCCCTTTGGGTCCCCTTCCTTTGTATGGGAGCTCTGTTTTCATGCTATTTCACTCT
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                                                                                CAACCCCCTTTGGGTCCCCTTTGTATGGCCCTCTGTTTTCACTCTATTTCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5' non coding, 3' pol gene, and 3' non coding sequences of HERV-W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2782 BP; 741 A; 767 C; 565 G; 709 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 522.6; DB 3;
Pred. No. 2e-151;
0; Mismatches 49;
                                                                                                                                                                                                                                 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAAAAAAA 635
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                                                                                                                                                                                                                                                                                                                                                             BP.
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90.4%;
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4atches 574; Conservative
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2386 GGTCGGCCAACTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAGAC 2445
                                                                                                                                                                                                                                                           The invention relates to identifying compounds which are modulators of syncytin expression. The syncytin modulators are useful in diagnosis and treatment of preeclampsia and gestational trophoblast disorders (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a compound for treating a subject with or at risk of developing preeclampsia, comprises determining whether the expression or activity of syncytin in the cell is modulated in the presence of a test
                                                                                        2446 AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCTTAAGCCTAGGTGGGAAGGTGACC
                                                                                                                                                                  421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATTGCCTG
                                                                                                                                                                                                                                                                                                                         481 AGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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                                               AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                      361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, syncytin, preeclampsia, gestational trophoblast disorder, choriocarcinoma, hydatiform mole, placental site tumour, abortion, envelope gene, human endogenous defective retrovirus, HERV-W, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2746 ATTABATCTTGCAACTGCAAAAAAAAAAAAAAAA 2780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAA 635
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/product= "Syncytin"
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930. .2546
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human syncytin cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAE14540.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Con the basis of the PBS t-RNA motif used for the classification of human choosenes are retrovirus (HERVS) the full length endogenous provirus which was been located on the long arm of human chromosene 7 (7021-22) has been designated HERV-W. The present invention describes proteins or peptides (I) having superantisen (SAS) activity comprising the ENV protein (ENV) of HERV-W, the present invention describes proteins or peptides (I) having superantisen (SU) and transmembrane (TM) sub-units. (I) of HERV-W sAg activity, and can be used in: vaccines; antisensetherapy; and HERV-W SAG activity-inhibitors. (I) and encoding DNA/RNA are useful for disposing multiple sclerosis (MS) or HERV-W-wassociated disporders. (I) are also useful for identifying suberances (and optionally recovering) capable of binding to a retroviral superantigen associated with MS, substances capable of blocking SAG activity and substances actable of blocking capable of generating or included to be capable of blocking capable of generating or included to be devoid of SAG activity, and substances against HERV-W retroviral SAG activity, and substances capable of blocking an immune response compensation of SAG activity, and substances against HERV-W retroviral SAG activity, capable of blocking transcription or translation of HERV-W retroviral superantigen for use in treating or translation of MS. (I) and nucleic acids encoding them are useful for the treatment and conservance of diagnosing autoimmune disease. The present sequence encodes the specifically claimed envelope protein of HERV-W designated G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human retrovirus HERV-W ENV proteins/peptides having superantigen activity useful for diagnosing and treating multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.3%; Score 522.6; DB 5; Length 2782; 90.4%; Pred. No. 2e-151; ive 0; Mismatches 49; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2782 BP; 741 A; 768 C; 564 G; 709 T; 0 U; 0 Other;
                /transl_except= (pos:2170. .2172,aa:Asn)
2380. .2782
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Fig 9; 94pp; English.
                                                                                                                                                                                                           30-OCT-2000; 2000WO-EP010659
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                                                                                                                                                                                                                                                                                                                                               Conrad B, Mach B;
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WO200194629-A2.
             Homo sapiens.
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
choriocarcinoma, hydatiform mole, placental site tumour and missed/
incomplete abortion). Syncytin is a human gene derived from the envelope
gene of human endogenous defective retrovirus, HERV-W. The present
invention is based partly on the discovery that syncytin expression is
dramatically reduced in precelampsia, and is also mis-localised to the
apical syncytiotrophoblast membrane. The present sequence is human
                                                                                                                                                               61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                                                                          -----CAAATGGAGCCCAAGATGCAGTCCAAGACTAAGATCTACGGAGACCC
                                                                                                                                                                                                                                          CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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                                                                                                                                                    CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATCAAAACTA
                                                                                                                                Gaps
                                                                                                                               12;
                                                                                                         Length 2930;
                                                                                     Sequence 2930 BP; 842 A; 800 C; 571 G; 717 T; 0 U; 0 Other;
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colon adenocarcinoma related gene sequence SEQ ID NO:81
                                                                                                          9
                                                                                                                                 41;
                                                                                                          Score 517.4; DB 6;
Pred. No. 8.3e-150;
                                                                                                                                0; Mismatches
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                                                                                                         81.5%;
ilarity 91.4%;
Conservative
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                                                                                                                       Similarity
                                                                syncytin cDNA
                                                                                                            Query Match
Best Local Simi.
Matches 564;
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The present invention describes a method (M1) for screening for an anti-
neoplastic agent. The method involves exposing cells to a chemical agent
to be tested for anti-neoplastic activity, determining a change in
expression of at least one gene (I) of a signature gene set, where (I)
comprises a sequence (S) selected from 8447 sequences (given in ABL61664
to ABL70110), or is at least 95% identical to (S), where a change in
expression is indicative of anti-neoplastic activity. (I) has cytostatic
activity and can be used in gene therapy. M1 can be used for screening an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change
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                                                                                 05-JUN-2000; 2000US-023313P.
18-SEP-2000; 2000US-023313P.
20-SEP-2000; 2000US-0234034P.
20-SEP-2000; 2000US-0234034P.
22-SEP-2000; 2000US-0234652P.
22-SEP-2000; 2000US-0234567P.
22-SEP-2000; 2000US-0234567P.
22-SEP-2000; 2000US-0234567P.
25-SEP-2000; 2000US-0234567P.
25-SEP-2000; 2000US-023563P.
25-SEP-2000; 2000US-023563P.
25-SEP-2000; 2000US-023563P.
25-SEP-2000; 2000US-023563P.
25-SEP-2000; 2000US-023563P.
25-SEP-2000; 2000US-023563P.
26-SEP-2000; 2000US-023563P.
27-SEP-2000; 2000US-023563P.
28-SEP-2000; 2000US-023563P.
28-SEP-2000; 2000US-023563P.
28-SEP-2000; 2000US-023603P.
28-SEP-2000; 2000US-023729P.
28-CCT-2000; 2000US-023729P.
28-CCT-2000; 2000US-023729P.
28-CCT-2000; 2000US-023729P.
28-CCT-2000; 2000US-023729P.
28-CCT-2000; 2000US-023729P.
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03-OCT-2000; 2000US-0237606P.
03-OCT-2000; 2000US-0237608P.
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30-MAY-2001; 2001WO-US010838
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multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diabetes;
anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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                                                                                                                                                                                            Gaps
                                                                                                                                     Sequence 56093 BP; 16164 A; 12346 C; 10702 G; 16881 T; 0 U; 0 Other;
                                                                                                                                                               Length 56093;
                                                                                                                                                                                            12;
                                                                                                                                                                                              Indels
                                                                                                                                                                  .2; DB 6;
8.3e-149;
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                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                    Score 516.2;
Pred. No. 8.3
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                                                                                                                                                                  Query Match 81.3%;
Best Local Similarity 91.1%;
Matches 564; Conservative
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                                                                                                                                                                                                                                                                                                               This sequence represents the complete sequence of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulin-dependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes associated with this susceptibility
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                                                                                                                                                                                                                                     New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7582 BP; 2156 A; 1877 C; 1537 G; 1796 T; 2 U; 214 Other;
marker;
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disseminated lupus erythematosus; pregnancy; chromosomal
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89.5%; Pred. No. 9.8e-148;
iive 11; Mismatches 42;
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                             retrovirus
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hes 552; Conservative
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                                                                                                                                                               (INMR ) BIO MERIEUX
                                Human endogenous
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The present sequence represents an endogenetic retrovirus, which is associated with an autoimmune disease, and is integrated into the human genome. The retrovirus is human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. HERV-W nucleic acid fragments, or proteins derived from it, are useful for disgnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6976 CCCTGTATCTTRACCTCCTTGTTAACTTTGTCTCTTCCAGAATCGAAGCTGTRAAACTA
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                                                                                                                                                                Sequence 7582 BP; 2156 A; 1876 C; 1538 G; 1796 T; 0 U; 216 Other;
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                                                                                                                                                                                             Length 7582;
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                                                                                                                                                                                                                          Indels
                                                                                                                                                                                             Score 511.4; DB 3;
Pred. No. 9.8e-148;
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Best Local Similarity 89.5
Matches 552; Conservative
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                                                                    CAACCCCCTTTGGGTCCCCTTTCCTATGGGAGCTCTGTTTTCATGTTTTCACTCT
                                       CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCT
                                                                                                                                                                                                                                                                                                                     Dimmune disease; retrovirus; human endogenous retrovirus W_i gene; pregnancy; multiple sclerosis; T cell proliferation;
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note= "U3-R of 3' LTR'
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note= "ORF1 env538"
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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening of bioactive agent capable cof binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for a bioactive agent capable of modulating the activity of CAP; (iv) for unititiating the activity of CAP; (vi) for treating carcinoma; (vii) for inhibiting the effect of CAP; (vii) for treating carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for (x) for diagnosing arctinoma or a propensity to carcinoma; and (xi) for carcinoma Lusella as DNA vaccines and the CAP are useful as dadition, the carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent capablished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100611 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAGTTGTAAAGCTA 100552
Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
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                                                                                                                                                                                                      CGGCAACGGCAACCCCCTTTGGGTCCCCTCTCTTTGTATGGGCGCTCTGTTTTCACTCTA
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                                                                                       TATTGCCTGAGAGCACAGGGGAGGGACAAGGATCGGGATATAAAACCCAGGCATTCGAGC
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                                                                                                                                                                                                                                                                                                                                                            33874 CTTCACTCTATTAAATATTGCAACTGCAAAAAAAAAAA 33912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; carcinoma; lymphoma; cancer; human; gene;
                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
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Pred. No. 7.7e-147;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 730; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACN44334 standard; DNA; 161334 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genomic sequence hCG32959
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Local Similarity 90.0%;
He 575; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002; 2002US-00087192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q. Regulatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immunor response, e.g. in immunotherapy. HERV-7q peptides and their coding sequences can be used in immunogenic or vaccinating compositions, for the protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid sequences of human endogenous retrovirus, HERV-7q, usdiagnosis, treatment and prevention of autoimmune and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 46340 BP; 16104 A; 8738 C; 8434 G; 13064 T; 0 U; 0 Other;
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Pred. No. 4.2e-147;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                        (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 15; Page 186-199; 225pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Rieger F;
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                                                                                                                                                                                                                                                                                                                     98FR-00007920
                                                                                          Human endogenous retrovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Perin J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-160587/14.
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575; Conserv
                                    multiple sclerosis;
                                                                                                                                                                                                                                                                                                                        23-JUN-1998;
                                                                                                                                                WO9967395-A1
                                                                                                                                                                                                                                                                  23-JUN-1999;
                                                                                                                                                                                                         29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                       Alliel PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10499 BP; 3048 A; 2676 C; 2280 G; 2495 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 10499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 505.8; DB 3;
Pred. No. 6.3e-146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                              3; Fig 1; 225pp; French.
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91.18;
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                                                        CAAATCGTTCTTCAAATGGAACCCCAGATGAAGTCCATGACTAAGATCTTCAAGGTCTACGTGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
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                                                                                                                                                            Cytostatic; carcinoma; lymphoma; cancer; human; gene;
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                                                                                                      Human genomic sequence hCG37193
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Matches 577; Conserv
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                                                                                                                                                                                                                            Homo sapiens.
                                                18-NOV-2004
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Claim 1; SEQ ID NO 4642; 639pp + Sequence Listing;
                                                                                              Human genome-derived single exon nucleic gene expression in human fetal liver.
                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                               Chen W,
      03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
7-SEP-2000; 2000US-0234559P.
04-OCT-2000; 2000CB-00024263.
2000US-00608408
                                                               Hanzel DK,
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                                                                                                                 CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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                                 Gaps
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                78.7%; Score 499.6; DB 4;
llarity 88.7%; Pred. No. 2.3e-144;
Conservative 0; Mismatches 54;
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26-MAY-2000; 2000US-0207456P.
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es 571; Conserv
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | CGGCAACGGCAACCCCCTTTGGGTCCCTCTTTGTTGGGCGCTCTGTTTCACTCTA 591
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78.7%; Score 499.6; DB 4; Length 1894;
Best Local Similarity 88.7%; Pred. No. 2.3e-144;
Matches 571; Conservative 0; Mismatches 54; Indels 19;
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New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
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                                                                                                                                                                                                                                  1457 TGTTGGCCAACCTCCCCAACAGCAGTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGA
                                                                                                                                                                                                                                                                                                                                                                CGGCAACGGCAACCCCCTTTGGGTCCCCTTTCTATGGGCGCTCTGTTTTCACTCTA
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                                                        AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                              AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Human breast cell single exon nucleic acid probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
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21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for prodicting a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1217 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTTCCAGAATCGAAGCAGTAAAACTA
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              Indels
                                                                                                                                                                                                                                                                                  microarray; human; placenta; antenatal diagnosis; disorder; ss.
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Best Local Similarity 88.7%; Pred. No. 2.3e-144;
Matches 571; Conservative 0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 4666; 654pp; English.
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, 2000US-0204456P.
, 2000US-00608408.
, 2000US-00632366.
, 2000US-0234687P.
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03-AUG-2000;
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27-SEP-2000;
04-OCT-2000;
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from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genemic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          472 TATTGCCTGAGAGCACAGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.7%; Score 499.6; DB 4; Best Local Similarity 88.7%; Pred. No. 2.3e-144; Matches 571; Conservative 0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
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                                      expression; heart; microarray; vascular system; probe;
lar disease; hypertension; cardiac arrhythmia;
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Pred. No. 2.3e-144;
0; Mismatches 54;
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30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0234559P.
04-OCT-2000; 2000GB-00024263.
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88.7%;
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Best Local Similarity 88.7
Matches 571; Conservative
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                                                                                                                                                                                                                                                               AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                               COGCAACOCCAACCCCCTTTGGGTCCCCTCTTTGTATGGGCGCTCTGTTTTCACTCTA
                                                                                                                                                                                                                                   AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC
                                                                                                                                                                                                                                                                                                                                                                                                 TATTGCCTGAGAGCACAGGGGAGGGACAAGGATCGGGATATAAAACCCAGGCATTCGAGC
                                                       CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                    CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                CTGGACCGGCCTGCTAGCCCCATGCTCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                          GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                      19;
Length 1894;
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  DB 4;
 Score 499.6; DB 4;
Pred. No. 2.3e-144;
0; Mismatches 54;
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26-MAY-2000; 2000US-0207456P.
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nilarity 88.7%;
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  Query Match
Best Local Similarity
Matches 571; Conser
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                 1576
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                                                                                 471
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    AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC
                                                                                             TATTGCTGAGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGC
                                                                                                                                         CGGCAACGGCAACCCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTCTA
                                                                                                                                                                                                                                                                                                                                                                                   Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                       GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC
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                                                                                                                                                                                          CAGCTACAGCTACCCTCTTTGGGTCCCCTCCCTTTGTATGGGAGCTCTGT
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053266.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult (C measuring human gene expression in a sample derived from human adult (Singh and Comprissing one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high c stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression (C in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, (hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS31005 represent human (C inver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                 Human, single exon nucleic acid probe; liver; cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
1807 CTTCACTCTATTAAATCTTGCAACTGCAAAAATAAAAATAGAAA 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 499.6; DB 4;
Pred. No. 2.3e-144;
0; Mismatches 54;
                                                                                                                                                                                                                             SEQ ID No 4660
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88.7%;
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26-MAY-2000; 2000US-0207456P-
30-JUN-2000; 2000US-00608408
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                                                                                                      DNA; 1894
                                                                                                                                                                                                                                                                                                              coronary heart disease; ss.
                                                                                                                                                                                    (first entry)
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                                                                                                                                              ABS29670;
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                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09
                                                                                                                                                                                                                                                  exon nucleic acid probes for analyzing gene expression in human
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Pred. No. 2.3e-144;
0; Mismatches 54; Indels 19;
                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO 4507; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
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                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
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      30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632566.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236359P.
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                                                                                       04-OCT-2000; 2000GB-00024263
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11, Conservative
                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                              WPI; 2001-483446/52
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe breast. The probes are useful for a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosling diseases of the human breast, staging and prognosling diseases of the human breast include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, prolliferative breast diseases of the breast, fibrocystic changes, prolliferative breast diseases of the breast by the present of diseases of the breast by the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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78.7%; Score 499.6; DB 5;
Best Local Similarity 88.7%; Pred. No. 2.3e-144;
Matches 571; Conservative 0; Mismatches 54;
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Sequence 108, App
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Sequence 15086, A
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1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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28 233.6 36.8 279 1 US-08-721-489-4 Sequence 4, Appliance 29 219.6 31.0 456 4 US-09-573-080A-21 Sequence 21. Appliance 31.0 456 4 US-09-51-976-9366 Sequence 21. Appliance 31.0 456 4 US-09-949-016-128750 Sequence 128750, Appliance 32.0 4 US-09-949-016-178750 Sequence 17057, Appliance 33.0 4 US-09-949-016-178750 Sequence 17057, Appliance 32.0 4 US-09-949-016-17896 Sequence 17057, Appliance 32.0 4 US-09-949-016-17896 Sequence 17057, Appliance 33.0 176.8 27.8 251672 4 US-09-949-016-17896 Sequence 11973, Appliance 33.0 176.8 27.8 25162 4 US-09-949-016-17896 Sequence 11973, Appliance 33.0 174.6 27.5 16652 4 US-09-949-016-13913 Sequence 11973, Appliance 32.0 174.4 27.4 39686 4 US-09-949-016-13413 Sequence 133.3 Appliance 32.0 174.6 27.5 16652 4 US-09-949-016-13413 Sequence 133.3 Appliance 32.0 174.6 27.6 42.0 174.2 27.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.4 43.0 174.2 174.3 174.4 43.0 174.2 174.4 43.0 174.2 174.3 174.4 44.4 175.2 174.4 43.0 174.2 174.3 174.4 44.4 175.2 174.4 43.0 174.2 174.3 174.4 44.5 174.4 44.5 174.4 44.5 174.4 44.5 174.4 44.5 174.4 44.5 174.4 44.5 174.5 174.4 44.5 174.5 174.4 44.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174.5 174
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## ALIGNMENTS

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US-06-979-947B-102

DESCRIPTION:

GENERAL:

GENERAL:

BESENG, FERENGE

BESTIN, FERENGE

SERVING MANDRAND;

FERENGE

TITLE OF INVENTION:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

NUMBER OF SCRUMENS:

CORRESPONDENCE ADDRESS:

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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1329;
                                                                                #1.30
                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA: e18/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: vUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 545; DB 4; 1
Pred. No. 7.2e-173;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-08-979-847B-108
                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION WINBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39(
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-836-6400
TELEFAX: 703-836-270
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                    LENGTH: 1329 base pairs
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                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 92.4%;
Matches 572; Conservative
ZIP: 22320
COMPUTER READABLE FORM:
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GARSON, JEREMY
TUKE, PHILIP
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULITPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
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                                                                                       CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                       CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGGCGGACCC
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   Length 635
                                  Indels
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 Score 635; DB 4;
Pred. No. 2e-203;
0; Mismatches 0;
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BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 108, Application US/08979847B
Patent No. 6582703
GENERAL INFORMATION:
APPLICANT: BERRON, HERVE
BESEME, FREDERIC
 Query Match
Best Local Similarity 100.0%;
Matches 635; Conservative 0
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US-08-979-847B-108
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Sequence 17382, Application US/09949016

Sequence 17382, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, U. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOLO1307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRESESEQ for Windows Version 4.0
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                                      2911 ATTAAATCTTGCAACTGCAAAAAAAAAAAAAAAAA 2945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.3%; Score 516.2; DB 4; 91.1%; Pred. No. 1.7e-162; ive 0; Mismatches 43;
              Query Match
Best Local Similarity 91.1
Matches 564; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                   RESULT 4
US-09-949-016-17382
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 17382
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                                                                                                                                                      APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Branes, David
APPLICANT: Mi Sha
APPLICANT: Mi Sha
APPLICANT: Mi Sha
APPLICANT: Mi Sha
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6006B.AJ172A
CURRENT APPLICATION NUMBER: US/09/175,928A
CURRENT FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 62
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84.1%; Score 533.8; DB 3; Length 2946;
Best Local Similarity 91.5%; Pred. No. 7.2e-169;
Matches 581; Conservative 0; Mismatches 42; Indels 12;
                                                                                                   Sequence 3, Application US/09175928A Patent No. 6312921 GENERAL INFORMATION:
||||||||| |||||||| || ATTAAATCATGCAACTGCA 875
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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                                                                       RESULT 3
US-09-175-928-3
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Sequence 1588, Application US/09949016
; Sequence 1588, Application US/09949016
; Patent No. 681233
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WINDER: US/09/949,016
    CURRENT PILING DATE: 2000-04-14
    PRIOR APPLICATION NUMBER: 60/241,755
    PRIOR APPLICATION NUMBER: 60/241,756
    PRIOR APPLICATION NUMBER: 60/231,498
    PRIOR PILING DATE: 2000-10-03
    PRIOR PILING DATE: 2000-10-03
    PRIOR PILING DATE: 2000-09-08
    NUMBER OF SEQ ID NOS: 207012
; SEQ ID NOS: 207012
; SEQ ID NOS: 207012
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Pred. No. 6e-160;
0; Mismatches 49; Indels 15;
                                                                       2746 ATTAAATCTTGCAACTG 2762
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Best Local Similarity 90.0%;
Matches 575; Conservative (
                                                        601 ATTAMATCTTGCAACTG
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US-09-949-016-15858/c
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                                                                                                                                                 Sequence Set0, Application US/09949016

| Sequence Set0, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VEWTER. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPRENCE: CLOU3.07
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| FILE REPRENCE: CLOU3.07
| CURRENT APPLICATION NUMBER: 60/24.755
| PRIOR APPLICATION NUMBER: 60/231,768
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SEQ ID NO 5640
| LEASTH: 2763
| LEASTH: 2763
           11459 CAACCCCTTTGGGTCCCCTCCCTTTGTATGGGAGCTCTGTTTTCATGCTATTTCACTCT 11518
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llarity 91.2%; Pred. No. 8.1e-163;
Conservative 0; Mismatches 42;
                                                                    Best Local Similarity
Matches 563; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
                                                                                                                                 RESULT 5
US-09-949-016-5640
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; Sequence 13002, Application US/09949016
; Batent No. 681239
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    FILE REPERENCE: CLOOL307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTHARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13002
; LENTH: 168394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(168394)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-13002
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Matches 534; Conservative
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LOCATION: (1)...(16839
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6180 CTATT 6176
                                                                               CTATT 593
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ORGANISM: Human
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Sequence 17411, Application US/09949016

Sequence 17411, Application US/09949016

Sequence 17411, Application US/09949016

Sequence 17411, Application US/09949016

GENERAL INFORMATION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOO1307

CURRENT FILING DATE: 2000-04-14

PRIOR PELING DATE: 2000-00-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17411

LENGTH: 99580
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CGGCAACGGCAACCCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTCTA 591
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Pred. No. 1.2e-140;
0; Mismatches 55; Indels 12;
                                                                                  92007 CITCACTCTATTAAATATTGCAACTGCAAAAAAAAAAA 91969
                                                                    Query Match
Best Local Similarity 88.9%;
Matches 538; Conservative
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RESULT 10

US-09-949-016-12249/c

US-09-949-016-12249, Application US/09949016

Sequence 12249, Application US/09949016

Sequence 12249, Application US/09949016

SEQUENCE 12249, Application US/09949016

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-20

PRIOR PELLING DATE: 2000-10-03

SPRIOR FILING DATE: 2000-10-03

SPRIOR PELLING DATE: 2000-10-03

SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NOS: 207012
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CATCAGCCAACCTCCCCAACAGCACTTGGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAC
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                                                                              ATCTATTGCCTGAGAGCACAGCGAGGACAAGGATCGGGATATAAACCCAGGCATTCG
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Pred. No. 3.4e-137;
0; Mismatches 54;
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LOCATION: (1)...(77997)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 88.9%;
Matches 538; Conservative C
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ORGANISM: Human
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US-09-949-016-17417/c

Sequence 17417, Application US/09949016

Sequence 17417, Application US/09949016

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOL01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 17417

LENGTH: 77772
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                                                                    CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 442.6; DB 4; Length 77772;
Pred. No. 3.4e-137;
0; Mismatches 54; Indels 13;
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i OTHER INFORMATION: n = A,T,C or
US-09-949-016-17417
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Best Local Similarity 88.9
Matches 538; Conservative
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US-09-394-016-13590/C

US-09-394-016-13590/C

Sequence 13590, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13590

LENTH: 149971
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                                                                                            256 AGGACTGACTGGATTTCCTAGGCCGACTAAGAATTCCTAAGCCTAGCTGGGAAGGTGACC 197
                                                                      GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGGACCAATC----- 411
                                                                                                                                                                                                         TATTGCCTGAGAGCACAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGC 531
                                                                                                                                                          181 GAAATCTCAACTGCACAACCCTACTATG-CCCCAATTCAGCGGGAAGCAGTT-AGAGCG
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Pred. No. 1.4e-111;
0; Mismatches 83;
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Best Local Similarity 80.9%;
Matches 529; Conservative
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; Sequence 44300, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    FILE REFERENCE: CLOOD.307
; CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; ROFTHARE: FRESE ESQUESCE OF WINDOWS VERSION 4.0
; SOUTHOW THE FRESE PRIOR FILING DATE: 2000-10-09
; SOUTHOW THE PRIOR PRIOR FILING DATE: 2000-10-09
; LENGTH: 601
              15437 AGCCGAATCGGGCAACCCTCTTTGGGTCCCCTCCGGTTGCATGGGAGCTCTGTTTTCACG 15378
                                                                               121 CTGGACCGGCCTGCTAGCCCCATGCTTAATGACATTGAAGGCACCCTCCCGAG 180
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Pred. No. 5e-126;
1; Mismatches 52;
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88.1%;
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Best Local Similarity 88.1
Matches 489; Conservative
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US-09-949-016-44300/c
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US-09-949-016-44300
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US-09-949-016-133739/c

| Sequence 133739, Application US/09949016
| Patent No. 6812339, Application US/09949016
| Patent No. 6812339, Application US/09949016
| Patent No. 6812319, Application In the Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company of Company o
174 CAGCCAGCAACGGCTACACTCTTTGGGTCCCCTCCCTTTATATGGGAGCTCTGTTTCCAC 115
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                                                                                                     CCCCTCCCTTTGTATGGGCGCTCTGTTTTCAC
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US-09-949-016-15393
US-09-949-016-15393, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION.
APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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pred. No. 1.2e-87;
1; Mismatches 25;
                                                                                                                                                                                                                                                              142157 TCTATTTCACTCTATTAAATCTTGCAACTGCA 142126
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US-09-949-016-133739
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Best Local Simi
Matches 306;
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General Information:
Sequence 1540/A

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                   8519 GTCGTCGGCCAACCTCCCCAACAGCACTTGAGTTTTCCTGTTGAGAGCCGAGACTGAGAG 18460
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                                                                                                                                                                                                          CTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGGACCAATC-----
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46.0%; Score 292; DB 4; Length 245286;
Best Local Similarity 92.5%; Pred. No. 4.2e-86;
Matches 307; Conservative 0; Mismatches 25; Indels 0;
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OTHER INFORMATION: n = A,T,C or
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; ORGANISM: Human
US-09-949-016-15086
                                                    TYPE: DNA
ORGANISM: Human
                                                                          ; OKGANISM: Human
US-09-949-016-44296
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Sequence 44296, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPREMENCE: CLOOU307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-01-0-3

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-09
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FEAST OF WINDOWS Version 4.0
SEQ ID NO 15393
LENGTH. 194790
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Pred. No. 8.1e-85;
0; Mismatches 70
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ilarity 82.6%;
Conservative
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Best Local Similarity
Matches 393; Conserv
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US-09-94-016-15086/C

Sequence 15086, Application US/09949016

Patent No. 6812339

Patent No. 6812339

Patent No. 6812339

TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR PLICATION NUMBER: 60/231,498

PRIOR PLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR SEQ ID NOS: 207012

SOFTWARE: PRESENCE for Windows Version 4.0

SEQ ID NO 15086

LENGTH: 219964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCT-GGGAAGGTGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCG
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                                                                                                                                                                                               Length 601;
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                                                                                                                                                                                               43.0%; Score 273.2; DB 4;
85.5%; Pred. No. 1.9e-81;
ive 1; Mismatches 49;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 44296
LENGTH: 601
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Matches 376; Conservative
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Best Local Similarity
Matches 281; Conserva
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RESULT 19
US-09-99-016-103638/c
j Sequence 103638 Application US/09949016
j Patent No. 681239
j GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
PRIOR REPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
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CAATCATCTATTGCCTGAGAGCACAGGGAGGACAAGGATCGGGATATAAACCCCAGGC
                                                                                                     Gaps
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Pred. No. 2.3e-74;
1; Mismatches 29;
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US-09-949-016-103639/c
; Sequence 103639, Application US/09949016
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86.3%;
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Best Local Similarity 86.3
Matches 308; Conservative
                                                                                                                                                                                                                                                                                                        TCACTCTATT 593
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; ORGANISM: Human
US-09-949-016-103638
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                    TGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACGAATCCCTAAGCTGGGA 352
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                                                AGGTGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCA
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NAME/KEY: rerpeat region
LOCATION: (1)..(780)
OTHER INFORMATION: ltr17
PUBLICATION INFORMATION:
AUTHORS: Jurka J; Walichiewicz, J; Milosavljevic, A
TITLE: Prototypic sequences for human repetitive DNA
VOLUME: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 385, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
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PAGES: 286-291
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US-09-573-080A-385
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US-09-573-080A-385
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Best Local S:
Matches 289
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US-US-149-ULD-149UB/C

) Sequence 14608, Application US/09949016

) Patent No. 6812339

) GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: LCD01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14608

LENGTH: 256287
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                                                                                                                                                                                  AATC-----AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAA 458
                                                                                                                                                                                                                                                                                                                                                                           392 AATCAGGTAGTAAAGAGAGCTCATTAAAATGCTAATTAGGGAAAAACAGGAAGTAAAGAA 333
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39.5%; Score 251; DB 4; Length 256287;
Best Local Similarity 86.3%; Pred. No. 2.9e-72;
Matches 308; Conservative 0; Mismatches 30; Indels 19;
                                                      39.5%; Score 251; DB 4; Length 601; 86.3%; Pred. No. 5.7e-74; Live 0; Mismatches 30; Indels
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14608
                                                             Query Match
Best Local Similarity 86.33
Matches 308; Conservative
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ORGANISM: Human
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US-09-949-016-103637
ORGANISM: Human
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Sequence 103637, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFRENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASESEQ for Windows Version 4.0
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR PILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTHARE PASSES OF WINDOWS VEFSION 4.0
SEQ ID NO 103639
LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 252.2; DB 4; Length Pred. No. 2.3e-74; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.3%;
Matches 308; Conservative
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US-09-949-016-103637/c
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; ORGANISM: Human
US-09-949-016-103639
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LENGTH: 601
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NAME/KEY: misc_feature

| LOCATION: (1)...(84571)

| OTHER INFORMATION: n = A,T,C or G

US-09-949-016-17420
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Best Local Similarity 99.4%;
Matches 303; Conservative
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US-09-949-016-17002
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APPLICAMT: VENTER, J. Craig et al.
APPLICAMT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREUESEQ FOR Windows Version 4.0
SEQ ID NO 44299
                                                                                                                               116237 GTAGCCAATCATCTGTCGCCTGAGAGCACAGGGGGGGGGACAATGATGATCAGGATATAAACC 116178
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                                                                                                                                                                                         CCGACCAATC-----AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGT
408 AATC-----AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAA
                                                      459 ATAGCCAATCATCTATTGCCTGAGAGCACAGGGAGGACAAGGATCGGGATATAAACC
                                                                                                               519 CAGGCATTCGAGCCGGCAACGGCAACCCCTTTGGGTCCCCTTCCCTTTGTATGGGCGCTC
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88.5%; Pred. No. 2e-73;
live 1; Mismatches 27;
                                                                                                                                                                                                                                                                        Sequence 44299, Application US/09949016 Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 39.3
Best Local Similarity 88.5
Matches 284; Conservative
                                                                                                                                                                                                                                               RESULT 23
US-09-949-016-44299/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
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RESULT 24 US-09-949-016-17420

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Sequence 17420, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANTY: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17420
LENGTH: 84571
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Sequence 17012, Application US/09949016
Patent No. 6812339
FACTOR OF GENERAL THORNANTION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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Pred. No. 8e-71;
0; Mismatches 22;
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65951 İdGGAAGGIGAICACAİTCAACCIITAAACAİGGGCIİACAAACIIAGCICACACACGACC 65892
                                                                                                                                    65891 AATCAGGTAGTAAAAGAGGCTCACTAAAATGCTAATTAGGCATAA--AGGAGGTAAAGAA 65834
                                                                                                                                                                                                      459 ATAGCCAATCATCTTTGCCTGAGAGCACAGGGGGGGGGACAAGGATCGGGGATATAAACC
                                                                                               408 AATCAG-----AGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAA
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APPLICANT: LaVallie, Edward
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
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COMPUTER: ISM PC comparible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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88.1%; Pred. No. 2.6e-68;
iive 1; Mismatches 32;
                 348 TGGGAAGGTGACTGCATCCACCTCTAAACATGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,878A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50, Application US/08686878A
Patent No. 5708157
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NAME: Brown, Scott A.
REGIGSTRATION UNMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                              65713 İGTİTİÇAÇİÇİATİ 65699
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Best Local Similarity 88.1
Matches 245; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: cDNA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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| Sequence 17068, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WIMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/241,756
| PRIOR PILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| WIMBER OF SEQ ID NOS: 207012
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 10-068
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ive 0; Mismatches 21
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                 ; NAME/KEY: misc_feature
; LOCATION: (1)...(140224)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17002
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Matches 283; Conservative
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.9<sup>3</sup>
Matches 285, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17068
                                                                                   TYPE: DNA
ORGANISM: Human
                                         SEQ ID NO 17002
LENGTH: 140224
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N: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATI.
30307
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                                                                                                                                                                   181 ceccaaccccititeserccccccrticiaidesecinicititicarectairican
                                                                                                                           537
                                                                                                                                                                                                            CGGCAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCAC 597
                                                                              61 NICANTAAATGATNATTNGGCAAAAACAGGGGAAAGAAATAGCAATCATCTATTGC 120
1 RCCACATCCACCTTTAAACACGGGGNTTGCAAANAAGATNACACTTGACCAATCAGAGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8304 ------CAAATGGAGCCCAAGATGCAGTCCAAGACTAAGATCTACCGCAGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8352 CridsAccidsCridcriadcccacdaricridaridardacarcaaldgcacciccridad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
                                           418 CICACIAAAAIGCIAAITAGGCAAAAAIAGGAGGIAAAAGAAAIAGCCAAICAICIAIIGC
                                                                                                                              CTGAGAGCACAGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
DATABASE ENTRY DATE:
DATABASE ENTRY DATE: 1996-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: repeat region
LOCATION: (1)..(8523)
OTHER INFORMATION: herv17
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
TITLE: Prototypic sequences for human repetitive DNA
JOURNAL: 35
                                                                                                                                                                                                                                                                                                                                    INTATTAAATNTTGCAACTGCAAAAAAAAAAAAAA 278
                                                                                                                                                                                                                                                                                                 TCTATTAAATCTTGCAACTGAAAAAAAAAAAAAAAAAA. 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 219.6; DB 4;
Pred. No. 1.2e-62;
0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JOAN, KNOLL
APPLICANT: ROGAN, PETER
TITLE OP INVENTION: SINGLE COPY GENOMIC FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
                                                                                                                                                                                                                                                                                                                                                                                                                                          gequence 21, Application US/09573080A, Patent No. 6828097, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 34.6%;
Best Local Similarity 87.7%;
Matches 256; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISSUE: 4
PAGES: 286-291
DATE: 1992-10-
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                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-573-080A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 8523
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SEQ ID NO 21
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                                                                                                                                61 NICANTAAATGATNATINGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTTTGC 120
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               ACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAG
                                             1 RCCACATCCACCTTTAAACACGGGGNTTGCAANAAGATNACACTTGACCAATCAGAGAG
                                                                                               418 CTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGC
                                                                                                                                                                                  CTGAGAGCACAGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAA
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APPLICANT: Racie, Liea
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spauding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                    CGGCAACCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTT
                                                                                                                                                                                                                                                                                                                                                   ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/721,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 233.6; DB 1;
Pred. No. 2.6e-68;
1; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION UNUBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08721489 Patent No. 5786465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.8%;
ilarity 88.1%;
Conservative
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LaVallie, Edward
Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: CDNA US-08-721-489-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 245; Conservat
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APPLICANT: Jacobs,
APPLICANT: MCCOY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 28
US-08-721-489-4
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 128750 LENGTH: 601
                                                                                          US-09-949-016-128750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
                                                          TYPE: DNA
ORGANISM: Human
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                                                                                                                            Query Match
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; Sequence 128750, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REPERENCE: CLOL01307
; CURRENT APPLICATION NUMBER: 00/241,755
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 CTGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 AAGGTGACCACATCCACCTTTAAGCAGGGGCTTGCAACTTAGCTCACACAGTC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAATCATCTATTGCCTGAGAGCACAGGGGGGGGGGACAAGGATCGGGATATAAACCCAGG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 AAGGTGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGACCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                8472 CGTCGGCCAACCTCCCCAACACTTAGGTTTTCCTGTTGAGATGGGGGAC 8523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                       APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9366
LENGTH: 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 196.6; DB 4;
Pred. No. 1.1e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                          US-09-621-976-9366/c; Sequence 9366, Application US/09621976; Patent No. 6639063; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.9%;
Matches 264; Conservative (
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CORGANISM: Homo sapiens
US-09-621-976-9366
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Sequence 17057, Application US/09949016

Sequence 17057, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, DOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

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PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498
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AAGGTGACTCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 ACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGTCATCAGCCA
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                                                                                                                                                          12;
Length 601;
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28.4%; Score 180.4; DB 4; Length 1
Best Local Similarity 82.1%; Pred. No. 1.3e-48;
Matches 271; Conservative 0; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420 CACTAAATGCTAATTAGGC-AAAAATAGGAGGTAAAGAAATAGCCAA
                                                                                                                                                          Indels
30.8%; Score 195.6; DB 4;
80.5%; Pred. No. 2.7e-55;
iive 1; Mismatches 55;
                                                                                              Best Local Similarity 80.5
Matches 280; Conservative
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Sequence 17296, Application US/09949016

| Sequence 17296, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VETYER, VETYER, VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | VETYER | 
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT PLICATION NUMBER: US/09/949,016
CURRENT FLING DATE: 2000-04-14
PRIOR PELING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR FLING DATE: 2000-10-03
PRIOR FLING DATE: 2000-10-03
PRIOR FLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASSEQ for Windows Version 4.0
SEQ ID NO 195792
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 GAAGGTGACTGCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCGGACCAAT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-----AGAGAGCTCACTAAAATGCTAATTAGGC-AAAAATAGGAGGTAAAGAAAT 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 CTGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCT-GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 AG-CCAATCATCTATTGCCTGAGAGCACGGGGGGGGACAAGGATCGGGATATAAAACC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.8%; Score 176.8; DB 4;
85.4%; Pred. No. 6e-49;
tive 0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.4'
Matches 270; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
US-09-949-016-195792
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US-09-949-016-17296
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FEATURE:
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US-09-949-016-44301/c
; Sequence 41301, Application US/09949016
; Patent No. 6812349
; GENERAL INFORMATION:
TITLE OF INVENTION: POLYMOREHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR PILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 44301
LENGTH: 601
                                                                              92354 AGGTAATAAAGAGAAGTCATTAAAATACCAATTAGGCTAAAAGCAGGAGGAGGTAAAGAAATA 92413
                                                                                                                                                                                                                                       182 CAAATTGTTCTTCAAATGGAGCCCCAGATGCAGTCCATGACTAAAATCTACTGCAGACCC 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 CCCTGTATACTTTAACATCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAGCTATAAAACTA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTA
                                                                                                                                     GCCAA-TCATCTATTGCCTGAGAGCACA-GCGGGAGGGACAAGGATCGGGATATAAACCC
                                                                                                                                                                                      92414 GrchAgrchTrarcGccrchGaGrbcacrGGGGGGGGGACAArGArGGAGGGATATAAACrc
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Pred. No. 2.4e-49;
0; Mismatches 25; Indels
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US-09-949-016-195792/c
; Sequence 195792, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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88.5%;
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Best Local Similarity 88.5
Matches 216; Conservative
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ORGANISM: Human
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VG=09-016-44310/c

VG=09-016-44310/c

VG=09-016-41310/c

VG=09-010-10-10/c

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Pred. No. 2.4e-48;
1; Mismatches 41;
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; Sequence 11973, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; TUREBRY APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PLING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                      292 CTGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCTTAGCT-GG
                                                                                                                                                                                                                                                                                                                                                                                                               351 GAAGGIGACIGCAICCACCICIAAACAIGGGGCIIGCAACTIAGCICACACCCGACCAAI
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                                                                                                                                 Length 251672;
                                                                                                                                                                                                     Indels
                                                                                                                             Score 176.8; DB 4;
Pred. No. 3e-47;
0; Mismatches 32;
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| LOCATION: (1)...(251682)

| OTHER INFORMATION: n = A,T,C or G

US-09-949-016-11973
// LOCATION: (1)...(251672)
// OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17296
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                                                                                                                                 Query Match 27.8*;
Best Local Similarity 85.4*;
Matches 270; Conservative
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US-09-949-016-11973
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Squence 11770, Application US/09949016
Squence 11770, Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYNORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-010-03
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                                                                                                                                                                                                                                                                                                                                                                                  Length 39686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Query Match

27.4%; Score 174; DB 4;
Best Local Similarity 83.1%; Pred. No. 7.9e-47;
Matches 261; Conservative 0; Mismatches 40
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13633
LENGTH: 39686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)... (49487)
; OTHER INFORMATION: n = A,T,C or US-09-949-016-11770
                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(39686)
CTHER INFORMATION: n = A,T,C or (1)...(1969-016-13633)
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ORGANISM: Human
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ORGANISM: Human
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                         Sequence 13413, Application US/09949016

| Sequence 13413, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION:
| APPLICANT' EVENTE, JO. Craig et al. APPLICANT' EVENTE, JO. Craig et al. APPLICANT' EVENTE, JO. Craig et al. TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLORO1307
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLORO1307
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT PILING DATE: 2000-04-14
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 13413
| LANGTH: 116652
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US-09-949-016-13633/C
US-09-949-016-13633, Application US/09949016
; Sequence 13633, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
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Pred. No. 1e-46;
0; Mismatches 34; Indels 14;
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US-09-949-016-13413
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Best Local Similarity 84.9%;
Matches 269; Conservative
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                         293 TGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCT-GGG 351
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0; Mismatches 40; Indels 13; Gaps
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February 21, 2005, 11:52:50 ; Search time 350.955 Seconds (without alignments) 10694.149 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                        OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                          Scoring table:
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Published Applications NA:\*

| cgn2\_6/ptodata/1/pubpna/USO7\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO7\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO6\_DNEW PUB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO6\_DNEW PUB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO6\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO6\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO8\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO8\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO8\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO9\_PUBCOMB.seq:\*
Database

Listing first 45 summaries

Post-processing: Minimum Match 0% Maximum Match 100%

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence 102, App	Sequence 102, App Sequence 18, Appl	Sequence 6792, Ap	Sequence 4, Appli	Sequence 108, App	Sequence 108, App	Sequence 910, App	Sequence 134, App	Sequence 3, Appli	Sequence 3, Appli
ID	US-08-979-847-102	US-10-114-104-102 US-10-637-565-18	US-10-719-993-6792	US-10-416-642-4	US-08-979-847-108	US-10-114-104-108	US-10-087-192-910	US-10-114-893-134	US-10-016-249-3	US-09-731-231A-3
DB		17	18	17	œ	16	13	13	15	0
% Query Match Length DB ID	635	2030	366710	2074	1329	1329	21646	2946	2946	326014
% Query Match	100.0	97.2	88.9	86.0	85.8	85.8	85.6	84.1	84.1	83.9
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FILING DATE: 26-NOV CLASSIFICATION: 435

3, 25, 170 126 126	1, Apr 81, 7 30, 7 730, 1666,	678 148 115, 114, 117, 718	Sequence 289680, Sequence 17699, A Sequence 47, Appl Sequence 8554, Ap Sequence 2175, Ap Sequence 224966, Sequence 183, App Sequence 183, App
US-10-751-985-3 US-10-632-793-25 US-10-719-993-7065 US-10-741-600-1795 US-10-719-993-6815 US-10-719-993-26	US-09-902-555-1 US-09-902-555-1 US-09-873-367C-81 US-10-632-793-30 US-10-087-192-730 US-10-087-192-1666 US-09-864-761-4444 US-10-632-793-28	US-10-276-774-678 US-09-997-722-148 US-10-220-120-15 US-10-104-047-1148 US-10-204-887-10 · US-10-220-120-17 US-10-198-846-9936 US-10-198-846-9936 US-10-027-632-289680	US-10-027-632-289680 US-10-466-531-47 US-10-466-531-47 US-10-029-386-8554 US-10-027-632-224966 US-10-027-632-224966 US-09-764-881-183 US-09-764-881-183 US-10-242-747-183
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## ALIGNMENTS

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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLAC
TITLE OF INVENTION: THERAPEUTIC PURPOSES
CORRESPONDENCES: 210
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: 979,847 FILING DATE: 26-NOV-1997
                                                                                        APPLICANT: BESEME, FREDERIC
APPLICANT: BESEME, FREDERIC
APPLICANT: BEDIN, FREDERIC
APPLICANT: PARANHOS-BACCALA, GLAUCIA
APPLICANT: KOMURIAN-PRADEL, FLORENCE
APPLICANT: MANDRAND, BERNARD
APPLICANT: GARSON, JERRENT
APPLICANT: TUKE, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
               Sequence 102, Application US/08979847 Publication No. US20030039664A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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COUNTRY: US/
ZIP: 22320
US-08-979-847-102
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, GLAUCIA FLORENCE COLETTE

PARANHOS-BACCALA, KOMURIAN-PRADEL,

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                                                                                                                                                                                                          Length 635,
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                                                                                                                                                                                                          Query Match 100.0%; Score 635; DB 8; 18est Local Similarity 100.0%; Pred. No. 2.4e-187; Matches 635; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTAAATCTTGCAACTGAAAAAAAAAAAAAAAA 635
                                           39046A
ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISFRATION NUMBER: 30,024

REFERENCE/COCKET NUMBER: WB 39,

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6410

TELEFHORE: 703-836-6410

TELEFAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 102:

SEQUENCE CHARACTERISTICS:

LENGTH: 635 base pairs

TYPE: nucleic acid

STRANDEDNESS: SINGle
                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                         linear
                                                                                                                                                                                       US-08-979-847-102
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Sequence 102, Application US/10114104
Publication No. US20030198647A1
GENERAL INPORMATION:
APPLICANT: PERRON, HERVE
BESEME, FREDERIC
BEDIN, FREDERIC

10-114-104-102

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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLECTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHY)
THERAPEUTIC PURPOSES
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                                                                                                                                                                                                                                                                                                                                                         MEDIUM ITER: FLOPEY GLEAD

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/114,104

FILING DATE: 03-Apr-2002

CLASSIFICATION NUMBER: 08/979,847

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/979,847

ATTORNEY/AGENT INFORMATION:

NAME: BERRAIGE, WILLIAM P.

REGERENTOS DOCKET NUMBER: 30,024

REFERRAITON NUMBER: 30,024

REFERRAITON NUMBER: 30,024

REFERRAITON NUMBER: 30,024

REFERRAITON STORY NUMBER: 30,024

TELEPHONE: 703-836-6400

INFORMATION: 703-836-6400
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100.0%; Pred. No. 2.4e-187;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | INTEGERAL OF SECTION |
| TYPE: nucleic acid |
| TYPE: nucleic acid |
| STRANDEDNESS: single |
| POPLOGY: linear |
| MOLECULE TYPE: cDNA |
| SEQUENCE DESCRIPTION: SEQ ID NO: 102: US-10-114-104-102
                                                                                                                                                                                            & BERRIDGE, PLC
                                                                                                                                                  NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSE: BERRIDG
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 2232
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
JOLIVET-REYNAUD, CC
MANDRAND, BERNARD
GARSON, JEREMY
TUKE, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 635; Conservative
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NAME/KEY: misc_feature
LOCATION: (1) ...(366710)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
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Sequence 6792, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
FADELICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOCTWAREE FASTESEQ FOR Windows Version 4.0
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1636 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGCTGAGAGAC
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                                                                         1696 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                   1756 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
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                                                        AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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88.9%; Score 564.8; DB 18;
Best Local Similarity 93.4%; Pred. No. 3.9e-164;
Matches 590; Conservative 0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1996 ATTAAATCTTGCAACTGAAAAAAAAAAAAAAA 2030
                                                                                                                                                                                                                                                                                                                                                                                                                                      601 ATTAAATCTTGCAACTGAAAAAAAAAAAAAA 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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US-10-719-993-6792/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6792
LENGTH: 366710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ÚS-10-719-993-6792
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US-10-637-565-18

US-10-637-565-18

Sequence 18, Application US/10637565

Publication No. US20040043381A1

GENERAL INFORMATION:

APPLICANT: PARANHOS-BACCALA, Glaucia

APPLICANT: PERRON, Herve

APPLICANT: PRENOW, Herve

APPLICANT: PRENOW PROBEL, Florence

TITLE OF INVENTION: THE LITE REGION OF MSRV-1 RETROVIRUS

TITLE OF INVENTION: METHODS FOR DETECTING MSRV-1 RETROVIRUS

TITLE OF INVENTION: WHBER: US/10/637,565

CURRENT APPLICATION NUMBER: US/10/637,565

CURRENT FILING DATE: 2003-08-11

PRIOR FILING DATE: 2000-02-15

PRIOR FILING DATE: 2000-02-15

PRIOR FILING DATE: 2000-02-15

PRIOR FILING DATE: 2000-02-15

PRIOR FILING DATE: 2000-02-15

NUMBER OF SEQ ID NOS: 20

SOUTHWARE: PALEARTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGACTGAGAGAC 300
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                                                                                                                                     480
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                                              361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
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Pred. No. 1.3e-181;
0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                            Query Match 97.2%;
Best Local Similarity 98.3%;
Matches 624; Conservative C
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; LOCATION: (1)
US-10-637-565-18
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LENGTH: 2030
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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
TITLE OF INVENTION: THERAPEUTIC PURPOSES
NUMBER OF SEQUENCES: 210
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1639 GAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCAGGAGGAGGAGTTAGAGCGGT
                                                                                             1759 AGGACTAGCTGGATTTCCTAGGCCGATTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACC
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APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 703-836-6400
TELEFAX: 703-836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 108, Application US/08979847
Publication No. US20030039664A1
GENERAL INFORMATION:
APPLICANT: BESEME, FREDERIC
APPLICANT: BESEME, FREDERIC
APPLICANT: PARAWHOS-BACCALA, GLAUCIA
APPLICANT: PARAWHOS-BACCALA, GLAUCIA
APPLICANT: JOLIVET-REYNAUD, COLETTE
APPLICANT: JOLIVET-REYNAUD, COLETTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PARANHOS-BACCALA, GI
APPLICANT: KOMURIAN-PRADEL, FLC
APPLICANT: JOLIVET-REYNAUD, COI
APPLICANT: MANDRAND, BERNARD
APPLICANT: GARSON, JEREMY
APPLICANT: TUKE, PHILIP
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STREET: P.O. BOX 19928
CITY: ALEXANDRIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Incyte ID No. US20040043452A1 7477736CB1
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APPLICANT: RAWKUMAR, Jayalaxmi
APPLICANT: RAWKUMAR, Jayalaxmi
APPLICANT: ARVIZU: Chandra
ATTILE CANT: ARVIZU: Chandra
TITLE OF INVENTION: BMBRYOGENESIS ASSOCIATED PROTEINS
FILE REFERENCE: PF-0842 PCT
CURRENT APPLICATION NUMBER: US/10/416,642
CURRENT FILING DATE: 2003-05-13
PRIOR APPLICATION NUMBER: 60/249,407
PRIOR APPLICATION NUMBER: 2000-11-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 546.4; DB 17;
Pred. No. 1.9e-159;
0; Mismatches 37;
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; OTHER INFORMATION: a, t, c, g, or other
US-10-416-642-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10416642
Publication No. US20040043452A1
GENERAL INFORMATION:
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93.8%;
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Best Local Similarity 93.8
Matches 579; Conservative
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LENGTH: 2074
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US-10-416-642-4
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 545; DB 16;
Pred. No. 4.3e-159;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,847
FILING DATE: 26-NOV-1997
ATTORNEY, AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE, DOCKET WUMBER: WPB 39046A
            THERAPEUTIC PURPOSES
OF SEQUENCES: 210
                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,104
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-114-104-108
                                                                  \Gamma
                                 NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE,
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1329 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 108: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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92.4%;
                                                                                                                                                            COMPUTER READABLE FORM:
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Best Local Similarity 92.4
Matches 572; Conservative
                                                                                                                              USA
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                                                                                                                                                 Length 1329;
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                                                                                                                                                                4.3e-159;
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                                                                                                                                                 85.8%; Score 545; DB 92.4%; Pred. No. 4.3e
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BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-RESYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JERBMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 108, Application US/10114104
Publication No. USZ0030198647A1
GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
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ATTAAATCATGCAACTGCA
      INFORMATION FOR SEQ ID NO: 10 SEQUENCE CHARACTERISTICS: LENGTH: 1329 base pairs TYPE: mucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                 Conservative
                                                                                                                                                                 Best Local Similarity
Matches 572; Conserv
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19991 ACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCACCTTTTGCCTG 20050
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GENERAL INCHMATION.

APPLICANT: Jacobs, Yenneth

APPLICANT: Lavalie, Edward R.

APPLICANT: Lavalie, Edward R.

APPLICANT: Collins-Racie, Lisa A.

APPLICANT: Collins-Racie, Lisa A.

APPLICANT: Benerics David

APPLICANT: Spanishing, Vikki

APPLICANT: Spanishing, Vikki

APPLICANT: Carlin-Duckett, McKeough

APPLICANT: Carlin-Duckett, McKeough

APPLICANT: Carlin-Duckett, McKeough

APPLICANT: Ganetics Institute, Inc.

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

FILE REFERENCE: GI 6000-10A

CURRENT FILING DATE: 2002-04-02

EARLIER FILING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 321

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 321
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                                    ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                      481 AGAGCACAGCGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
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Best Local Similarity 91.5%; Pred. No. 1.9e-155;
Matches 581; Conservative 0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                  Sequence 134, Application US/10114893; Publication No. US20020193567A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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            677 ACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCCAATCATTTTGCCTG 736
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Best Local Similarity 94.8%; Pred. No. 5e-158;
Matches 562; Conservative 0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                                                              Sequence 910, Application US/10087192
; Sequence 910, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
    APPLICANT: Morris, David W.
    APPLICANT: Engelhard, Eric K.
    TITLE OF INVENTION: OANCER
    TITLE OF INVENTION: CANCER
    TITLE OF INVENTION: OANCER
    FILE REFERENCE: 52045200012.
    CURRENT APPLICATION NUMBER: US/10/087,192
    CURRENT FILING DATE: 2002-03-01
    PRIOR PILING DATE: 2000-12-22
    PRIOR FILING DATE: 2001-03-02
    NUMBER OF SEQ ID NOS: 2059
    NUMBER OF SEQ ID NOS: 2059
    SOFTWARE: FRAELSEQ for Windows Version 4.0
    SEQ ID NO 910
    LENGTH: 21646
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NAME/KEY: misc_feature

LOCATION: (1)...(21646)

CTHER INFORMATION: n = A,T,C or G
US-10-087-192-910
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ORGANISM: Homo sapiens
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US-10-087-192-910
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Sequence 3, Application US/09731231A

Patent No. US20020082189A1

GENERAL INFORMATION:

TITLE OF INVENTION: ISCLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/731,231A

CURRENT APPLICATION NUMBER: US/09/731,231A

CURRENT FILING DATE: 2000-12-07

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FeatSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 326014
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1851 CAACCCCTTTGGGTCCCCTTTGTATGGGAGCTCTGTTTTCATGCTATTTCACTCT 2910
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83.9%; Score 532.8; DB 9;
Best Local Similarity 90.5%; Pred. No. 3.6e-154;
Matches 583; Conservative 0; Mismatches 52;
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; OTHER INFORMATION: n = A,T,C or
US-09-731-231A-3
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NAME/KEY: misc_feature
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ORGANISM: Human
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APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
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APPLICANT: Treacy, Maurice
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     GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACACGGACCAATCAGAGGTCC
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Pred. No. 1.9e-155;
0; Mismatches 42; Indels
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91.5%;
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Best Local Similarity 91.5
Matches 581; Conservative
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US-10-016-249-3
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; Sequence 25, Application US/10632793
; Publication No. US20040048298A1
; GENERAL INFORMATION:
    APPLICANT: PARAMNOS-BACCALA, Glaucia
    APPLICANT: PARAMNOS-BACCALA, Glaucia
    APPLICANT: WOISSET, Cecile
    TITLE OF INVENTION: ENDOGRENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN TITLE OF INVENTION: ENDOGRENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT;
    TITLE OF INVENTION: AUTOIMMUNE 1058A5, 193
    CURRENT FILING DATE: 2003-08-04, PRIOR PLICATION NUMBER: PCT/FR00/00144
    PRIOR PLICATION NUMBER: PCT/FR00/00144
    PRIOR PLILNG DATE: 2000-01-21
    PRIOR APPLICATION NUMBER: FCT/FR00/00144
    PRIOR PLILNG DATE: 1999-01-21
    PRIOR PLILNG DATE: 1999-01-21
    NUMBER OF SEQ ID NOS: 33
    SOFTHARE: PATENTIN OFFICE ACID NOS: 33
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                                                     GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATC------
                                                                                                                   412 AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC
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                                                                                                                                                                                                                                                                                                                                   82.8%; Score 525.8; DB 17; Length 90.7%; Pred. No. 3.9e-153; tive 0; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.77
Matches 576; Conservative
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US-10-632-793-25
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                                                                                                                                                                                                                                                                            Sequence 3, Application US/10751985
; Publication No. US20040126861A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REPRENCE: CLOO1007CON
; CURRENT FILING DATE: 2004-01-07
; UNRENT FILING DATE: 2004-01-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASESEQ for Windows Version 4.0
; SEQ ID NO 3
; SEQ ID NO 3
; LENGTH. 326014
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                                                                                                                                                                                             472 TATTGCCTGAQAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGC
                                                                                                                                                                                                                                                           CGGCAACGGCAACCCCCTTTGGGTCCCCTTCGTATGGGCGCTCTGTTTCACTCTA
                                                                                                                               AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATC
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83.9%; Score 532.8; DB 18;
Best Local Similarity 90.5%; Pred. No. 3.6e-154;
Matches 583; Conservative 0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(326014)
OTHER INFORMATION: n = A,T,C or G
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US-10-751-985-3/c
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NAME/KEY: misc_feature
LOCATION: (1)...(283351)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
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Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17995
LEMETH: 283351
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                                                    CGAAGAATCCCTAAGCCTAGCTGGAAGGTGACTGCATCCACCTCTAAACATGGGGCTTG
                                                                                                                                                                                        507 GGGATATAAACCCAGGCATTCGAGCCGGCAACGGCAACCCCCTTTGGGTCCCCTTTT
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ORGANISM: Homo sapiens
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OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASSOCIATED WITH METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174925 CAATGTTAATGACATGGAAGGCACCTTCCGGAGGAAATCTCAACTACACAACACCTACT 174984
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                                                                                             481 AGAGCACAGCGGAGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
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                             CGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAGAAC
                                                                         AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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Publication No. US20040265849A1
GENERAL INFORMATION:
TETLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE REFERENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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LENGTH: 283351
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US-10-719-993-7065
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US-10-719-993-7065
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(see Tables 1-
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US-10-741-600-17676
US-10-741-600-17676
Application No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFRENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT EILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17676
LENGTH: 1980090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 CGATGTTAATGACATTGAAGGCACCCCTCCCGAGGAAATCTCAAACTGCACAACCCCTACT
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                                                                                                                                                                                                       27 GTTTGTCTTCCAGAATCAAAACTGTAAAACTACAAATTGTTCTTCAAATGGAGCACCA
                                                                   CAACTTAGCTCACACCCGACCAATCAGAGCTCACTAAAATGCTAAATTAGGCAAAAATA
                                                                                                                              447 GGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGAGCACAGCGGAAGGGACAAGGATC
                                                                                                                                                                                        or insertion/deletion polymorphism
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              CGAAGAATCCCTAAGCTAGCTGGGAAGGTGACTGCATCCACCT
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Pred. No. 1.1e-150;
1; Mismatches 33; 1
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| LOCATION: (1)...(1980090)

| OTHER INFORMATION: n = A,T,C or G,

US-10-741-600-17676
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93.4%;
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Best Local Similarity 93.4
Matches 568; Conservative
                                                                                                                                                                                                                                                                                                                                            1777677 AAAAAAA 1777684
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| LOCATION: (1)...(1980090)

| OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-719-993-6815
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                                                                                         CAACTTAGCTCACACCCGACCAATCAGAGGCTCACTAAAATGCTAATTAGGCAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: GRNETIC POLYMORPHISMS ASS
TITLE OF INVENTION: GRNETIC POLYMORPHISMS ASS
TITLE OF INVENTION: ALZHEIMER'S DISEASE, ME'
FILE REPERBNCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILLING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FASTSEQ FOR WINGOWS Version 4.0
SEQ ID NO 6815
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6815, Application US/10719993 Publication No. US20040265849A1 GENERAL INFORMATION:
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US-10-719-993-6815
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481 AGAGCACAGCGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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                                                          AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                   361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
                                                                                                                                                                                                           ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAAAAGCCAATCATCTATTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10133036
; Beduence 1, Application US/10133036
; Publication No. US20040054133A1
; GENERAL INFORMATION:
    APPLICANT: Conrad, Bernard
; APPLICANT: Mach, Bernard
; TITLE OF INVENTION: Multiple Sclerosis-Related Superantigen
; FILE REFRENCE: 23135-507
; CURRENT APPLICATION NUMBER: US/10/133,036
; CURRENT FILING DATE: 2002-04-26
; PRIOR PELING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE PELING USE: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.0%; Score 521; DB 17; Length 2782; Best Local Similarity 90.2%; Pred. No. 1.9e-151; Matches 573; Conservative 0; Mismatches 50; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2746 ATTABATCTTGCAACTGCAAAAAAAAAAAAAAA 2780
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; ORGANISM: Human endogenous retrovirus
US-10-133-036-1
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                                           1777383 CTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACCGCATCCACCTTTAAACACGGGGCTTG 1777442
                                                                                                       JOURNALL LINCOLANT: PARANHOS:

APPLICANT: PARANHOS:
APPLICANT: PARANHOS:
APPLICANT: MALLET, Francois
APPLICANT: WALLET, Francois
APPLICANT: WOISSET, Cecile
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
FILE REFERENCE: 110048
CURRENT APPLICATION NUMBER: US/10/659,927
PRIOR APPLICATION NUMBER: US/09/669,927
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 1999-01-21
PRIOR PILING DATE: 1999-01-21
PRIOR FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
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Pred. No. 5.9e-152;
0; Mismatches 49; Indels 12;
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; Publication No. US20040048298A1
; GENERAL INFORMATION:
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1777677 AAAAAAA 1777684
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Matches 574; Conservative
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; ORGANISM: Homo sapiens
US-10-632-793-26
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APPLICANT: Soppet, Daniel
APPLICANT: Soppet, Daniel
APPLICANT: Soppet, Daniel
APPLICANT: Bodget, Daniel
APPLICANT: Endress, Gregory
APPLICANT: Endress, Gregory
APPLICANT: Endress, Gregory
APPLICANT: Carter, Reinhard
APPLICANT: Carter, Reinhard
APPLICANT: Carter, Reinhard
APPLICANT: Carter, Reinhard
APPLICANT: Carter, Renneth
TITLE OF INVENTION: Signature Gene Sets
TITLE OF INVENTION: Signature Gene Sets
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: U.S. 60/236,891
PRIOR PLIING DATE: 2000-09-29
PRIOR PLIING DATE: 2000-09-29
PRIOR PLIING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR PLIING DATE: 2000-11-01
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SPRO IN SEQ ID NOS: 1067
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541 CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGCCCCTCTGTTTTCACTCTATTTCACTCT
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                                                                        301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 81, Application US/09873367C; Publication No. US20030165839A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-09-873-367C-81
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                                                                                                                361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
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Best Local Similarity 91.4%; Pred. No. 2.5e-150;
Matches 564; Conservative 0; Mismatches 41;
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; NAME/KEY: CDS
; LOCATION: (930) ... (2546)
US-09-902-535-1
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US-09-902-535-1
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80.5%; Score 511.4; DB 17; Length
Best Local Similarity 89.5%; Pred. No. 3e-148;
Matches 552; Conservative 11; Mismatches 42; Indels
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NAME/KEY: misc_feature
LOCATION: (2213)..(2213)
OTHER INFORMATION: n = a or
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LOCATION: (3787)..(3787)
OTHER INFORMATION: n = a or
              NAME/KEY: misc feature
LOCATION: (1309)..(1309)
OTHER INFORMATION: n = a or
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NAME/KEY: misc_feature
LOCATION: (4115)..(4115)
OTHER INFORMATION: n = a or
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NAME/KEY: misc_feature
LOCATION: (1331)..(1331)
OTHER_INFORMATION: n = a
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SEQUENCE 30, Application US/10632793

FUBLICATION NO. US200400482981

GENERAL INFORMATION:

APPLICANT: PARANHOS-BACCALA, Glaucia

APPLICANT: MALLET, Francois

APPLICANT: MOISSET, Cecile

TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN TITLE OF INVENTION: AUTOHOMED DISEASE, LABELING METHOD AND REAGENT FILE REFERENCE: 110048

CURRENT APPLICATION NUMBER: US/10/632,793

CURRENT FILING DATE: 2003-08-04

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 1999-01-21

NUMBER OF SEQ ID NOS: 33

SOSTWARE: PATCHIN VERSION 3.1
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                                                                            37442 GAAATCTCAGCTGCACAACCTCTACTACGCCCCAATTCAGCAGAAGCAGTTAGAGCGT 37501
                                                                                                                               37502_CGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAGAC 37561
                                                                                                                                                                                          37622 ACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTGACCAATCAGAGAGGTC 37681
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                                                                                                                                                                        301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGAAGGTGACT
                                                                                                                                                                                                                                                                                                    421 ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG
                                                                                                                                                                                                                                                                                                                                                                  481 AGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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LOCATION: (355)..(355)
OTHER INFORMATION: n = a or g
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LOCATION: (1987..(198)
OTHER INFORMATION: n = a or g
FEATURE:
NAME/KRY: misc feature
LOCATION: (3077..(307)
OTHER INFORMATION: n = a or g
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LENGTH: 7582
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179846 CGGCATCCATTAAACACGGGGCTTGCAACTTAGCTCACACCGACCAATCAGGGAGT 279905
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                          CGGCAACGGCAACCCCCTTTGGGTCCCCTTTGTATGGGCGCTCTGTTTTCACTCTA 591
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78.9%; Score 500.8; DB 13; Length
Best Local Similarity 89.3%; Pred. No. 3.3e-144;
Matches 577; Conservative 0; Mismatches 57; Indels
                                                                                             630
                                                                                                                                                                                  US-10-087-192-1666;
Sequence 1666, Application US/10087192
Sequence 1666, Application US/10087192
Sequence 1666, Application US/10087192
Sequence 1666, Application US/10087192
Sequence 1666, Application US/202018286A1
Septication No. US202018286A1
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
FILE REFERENCE: 299452001122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
SPIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                            | NAME/KEY: misc_feature
| LOCATION: (1)...(285020)
| OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1666
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LENGTH: 285020
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80.4%; Score 510.6; DB 13; Length 161334;
Best Local Similarity 90.0%; Pred. No. 2.2e-147;
Matches 575; Conservative 0; Mismatches 49; Indels 15; G
                                                                                                                WESULT 43
US-10-087-192-730/C

Sequence 730, Application US/10087192
PUBLICATION No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: MOOFIL OWNORL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: ANOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: ANOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: ANOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR PILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SEQ ID NO 730
LENGTH: 161334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               // NAME/KEY: misc_feature
// LOCATION: (1)...(161334)
// OTHER INFORMATION: n = A,T,C or G
US-10-087-192-730
                                  601 ATTAAATCTTGCAACTG
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Sequence 28, Application US/10632793

Sequence 28, Application No. US20040048298A1

Sequence 28, Application No. US20040048298A1

GENERAL INFORMATION:

APPLICANT: PARANHOS-BACCALA, Glaucia

APPLICANT: WALLET, Francois

APPLICANT: WOLSET, Cecile

TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT

FILE REFRENCE: 11004 UNMBER: US/10/632,793

CURRENT APPLICATION NUMBER: US/10/632,793
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                  Length 1894;
D IN HELIOO, SIGNAL = 6

D IN HEART, SIGNAL = 5.4

D IN BITATY, SIGNAL = 5.9

D IN PETAL LIVER, SIGNAL = 6.7

D IN ADULT LIVER, SIGNAL = 6.7

D IN BORE MARNOW, SIGNAL = 6.3

D IN BOLE MARNOW, SIGNAL = 6.3

D IN HELA, SIGNAL = 7.2
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Best Local Similarity 88.7%;
Matches 571; Conservative
OTHER INFORMATION: ES OTHER INFORMATION: ES OTHER INFORMATION: ES OTHER INFORMATION: ES OTHER INFORMATION: ES OTHER INFORMATION: ES OTHER INFORMATION: ES OTHER INFORMATION: ES OTHER INFORMATION: ES
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Sequence 4444, Application US/0864761

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                                                          279966 TCTATCGCCTGAGAGCAC-GAGGAGGGACAATGATCAGGATATAAACCCAGGCATTCAA
                                                                                                                                                      GCCGGCAGTGGCTACCCGCTTTGGGTCCCCTCTGTTTGTATGGGAGCTCTGTTTTCACTC
                                TCTATTGCCTGAGAGCACAGCGGAGGGACAAGGATCGGGGATATAAACCCAGGCATTCGA
                                                                                                                        GCCGGCAACGCCAACCCCCTTTGGGTCCCCTTCCCTTTGTATGGGCGCTCTGTTTTCACTC
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ORGANISM: Homo sapiens
PEATURE:
OTHER INFORMATION: MAP TO AC002146.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =
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Sequence 148, Application US/08997722;
Publication No. US20040072154A1
GENERAL INFORMATION:
PAPLICANT: Morris, David
APPLICANT: Engelhard, Exic
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
TITLE REFERENCE: A-71171/RMS/DCF;
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
FRIOR PELLING DATE: 2000-12-22
FRIOR PELLING DATE: 2000-12-22
FRIOR PELLING DATE: 2001-03-02
FRIOR PELLING DATE: 2001-03-02
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Pred. No. 7.7e-143;
0; Mismatches 43;
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ilarity 91.2%;
Conservative C
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 678
                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-10-276-774-678
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nes 549; Conser
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Publication No. US20040053245A1
Publication No. US20040053245A1
Publication No. US20040053245A1
Publication No. US20040053245A1
APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TILE OF INVENTION: NO. US20040053245A1e1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2000-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
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Pred. No. 1.7e-143;
0; Mismatches 44;
            PRIOR APPLICATION NUMBER: US/09/869,927
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: PCT/FR00/00144
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 28
LENGTH: 3372
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Best Local Similarity 92.2%;
Matches 522; Conservative
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CORGANISM: Homo Bapiens
US-10-632-793-28
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60/184,770; 60/184,774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GATGCAGTCTATGACTAAGATCTACCACAGACCCTTGGACCGGCCTGCTAGCCCATGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:

NAMEKEY: misc_feature

) OTHER INFORMATION: Incyte ID No. US20040048253Al LG:429446.1:2000FEB18

US-10-220-120-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 GATGGAGTCCATGACTAAGATCCACCGTGGACCCCTGGACCGGCCTGCTAGCCCATGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HODGSON, David M.
APPLICANT: HODGSON, David M.
APPLICANT: LINCOLN, Steath B.
APPLICANT: JACKSON, Stuart
ITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PT-1113 PCT
CURRENT APPLICATION NUMBER: US/10/220,120
CURRENT FILING DATE: 2002-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.8%; Score 481.4; DB 17; Length
89.1%; Pred. No. 2.5e-139;
tive 0; Mismatches 56; Indels
                                                                                                                                                                                        ROSEN, Bruce H.
RUSSO, Frank D.
STOCKDREHER, Theresa
                                                                    FOOK, Willy T. GREENAWALT, Lila B. HILLMAN, Jennifer L. JONES, Anissa L.
                                                                                                                                                                                                                                                                  WRIGHT, Rachel J.
YAP, Pierre E.
YU, Jimmy Y.
BRADLEY, Diana L.
BRATCHER, Shawn R.
DAM, Tam C.
DANIELS, Susan E.
DUFOUR, Gerard E.
FLORES, Vincent
                                                                                                                                                     LIU, Tommy F.
ROSEBERRY, Ann M.
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COHEN, Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                    DAFFO, Abel
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Best Local
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                                                                                                                                                                                                                                                                                                               61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299
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                                                                                                                                                                                                                                                            5655 CCCTGTACCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCGAAGCTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                       CTGGACCGGCCTGCTAGCC-CATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 TCATCAGCCAACCTCCCCAACAGCACTTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGA
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                                                                                                                                                                                                                                    1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTA
                                                                                                                                                         DB 11; Length 22436;
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                                                                                                                                                                                                  69
                                                                                                                                                       Score 482.6; DB 11
Pred. No. 4.8e-139;
0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/10220120 Publication No. US20040048253A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: PANZER, Scott R.
APPLICANT: SPIRO, Peter A.
APPLICANT: SIMH, Purvi
APPLICANT: GHALUP, Michael S.
APPLICANT: CHALUP, Michael S.
APPLICANT: CHEN, Alice
APPLICANT: CHEN, Alice
APPLICANT: D'SS, Steven A.
APPLICANT: MSHBY, Stefan
APPLICANT: AMSHBY, Stefan
APPLICANT: DAHL, Christopher R.
                                                                                                                                                         76.0%;
87.6%;
    NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1
                                                                                                                                                         Query Match
Best Local Similarity 87.6'
Matches 565; Conservative
                                                                                TYPE: DNA
CORGANISM: Homo sapiens
US-09-997-722-148
                                          SEQ ID NO 148
LENGTH: 22436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-220-120-15
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147 CGATGTTAATGACATTGAAGGCACCCCTCCCGAGGAATCTCAACTGCACACACCCCTACT

241

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207 ATGCCCCAATTCAGCGGGAAGCAGTTAGAGCGGTCATCAGCCAACCTCCCCAACAGCACT 

360

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APPLICANT: STOCKARATE, INTEREST.

APPLICANT: BAFO. Abel
APPLICANT: WRIGHT, Rachel J.
APPLICANT: WRIGHT, Rachel J.
APPLICANT: WAS Pierr E.
APPLICANT: YAP, Pierr E.
APPLICANT: YAP, Pierr E.
APPLICANT: BRADLEY, Diana L.
APPLICANT: GHEN, Wensheng
APPLICANT: GHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: LINCOLN, Stephen E.
APPLICANT: LINCOLN, SECRETORY MOLECULES
FILE REFERENCE: PT-1134 PCT
CURRENT PILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: 06/185,215; 60/205,232; 60/205,323; 60/205,287;
CURRENT FILING DATE: 2000-02-24; 2000-05-17; 2000-05-17;
PRIOR PILING DATE: 2000-02-24; 2000-05-17; 2000-05-17;
NUMBER OF SEQ ID NOS: 159
SOFTWARE: PERL PROGram
                    1856 GGGGGGGAATGATGATGATGATGATATAAACTCAGGCATTCAAGCCAAGGAATGGCTACCCACT 1915
                                                                                                                                                                                                                                                    TIGGGICCCCTCCCTTIGIAIGGCGCTCTGTTTTCACTCTATTTCACTCTATTAAAICT 609
                                                                                                                                                      490 cgggaggaachaagaaTcGggaTaTaaacccagGcaTTcGagccGgcaacGgcaacccTT
                                                                           430 CTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGAGCACAG
379 GGGGCTTGCAACTTAGCTCACACCCGACCAATC-----AGAGAGCTCACTAAAATG
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                                                                                                                                                                                                                                                                                                                   610 TGCAACTGAAAAAAAAAAAAAAAA 635
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SQUENCE 10, Application US/10204887
PUBLICATION NO. US20030124569A1
GENERAL INFORMATION:
APPLICANT: BANVILLE, Steven C.
APPLICANT: SPIRO, Peter A.
APPLICANT: SHAN, Purvi
APPLICANT: GHAUD, Michael S.
APPLICANT: GHAUD, Michael S.
APPLICANT: GHAUD, Michael S.
APPLICANT: GHAUD, Simon C.
APPLICANT: GHAUD, Alice
APPLICANT: GHAUD, Simon C.
APPLICANT: DANIERS, Stefan
APPLICANT: DANIERS, Stefan
APPLICANT: DANIERS, Stefan
APPLICANT: DANIERS, Stefan
APPLICANT: PONICW, Gerard E.
APPLICANT: PONICW, Gerard E.
APPLICANT: FLORES, VINCENT
APPLICANT: FLORES, VINCENT
APPLICANT: PONG, Willy T.
APPLICANT: GREENAMALT, Lila B.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: JONES, ANISSA L.
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STOCKDREHER, Theresa K.
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ROSEBERRY, Ann M.
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LENGTH: 1564
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78
                                                                                                                                                                                                                                                                                                                                                         CAACTTAGCTCACACCCGACCAATCA-----GAGAGCTCACTAAAATGCTAATTAG 437
                                                                                                                                                                                                 GCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGAGCACAGCGGAGGG 497
                                                                                                                                                                                                                                                                      498 ACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGGCAACCCCTTTGGGTCC 557
                                        CGAAGAATCCCTAAGCCTAGGTGGAAGGTGACTGCATCCACCTCTAAACATGGGGGTTG 386
                                                                                                                     558 CCTCCTTTGTATGGGGGGTCTGTTTCACTCTATTCACTCTATTAAATCTTGCAACT 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1148, Application US/10104047
; Sequence 1148, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
    TITLE OF INVENTION:
    TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
    TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
    TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
    FILE REFERENCE: H1-A0105
    CURRENT APPLICATION NUMBER: US/10/104,047
    CURRENT APPLICATION NUMBER:
    PRIOR FILING DATE:
    PRIOR FILING DATE:
    NUMBER OF SEQ ID NOS: 4096
    SOFTWARE: PatentIN Ver. 2.1
    SEQ ID NO 1148
    LENGTH: 2349
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Pred. No. 2.5e-134;
0; Mismatches 75; Indels
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Best Local Similarity 86.4%;
Matches 541; Conservative 0
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CORGANISM: Homo sapiens
US-10-104-047-1148
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60/184,770; 60/184,774
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HODGSON, David M.
APPLICANT: LINCOLN, Stephen E.
APPLICANT: LINCOLN, Stephen E.
APPLICANT: LINCOLN, Stephen E.
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APPLICANT: LINCOLN, Stephen E.
APPLICANT: LINCOLN, Stephen E.
CURRENT ILILE OF INVARION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PILICATION NUMBER: US/10/220,120
CURRENT FILLE OF INVARION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILLE OF INVARION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILLE OF INVARION WINDER: US/10/220,120
CURRENT FILLE OF INVARION MUMBER: 60/184,777; 60/184,773; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/185,215; 60/204,204; 60/204,204; 60/204,204; 60/205,215; 60/205,215; 60/205,215; 60/205,215; 60/205,215; 60/205,215; 60/205,224; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 AAACTGTAAAACTACAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No. US20040048253A1 LI:351965.1:2000FBB01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 446.2; DB Pred. No. 3e-128; 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t, c, g, or other
                                                                                                                                                             χ.
                                                                                                         ROSEN, Bruce H.
RUSSO, Frank D.
STOCKDREHER, Theresa
                                                                                                                                                                                                               WRIGHT, Rachel J.
YAP, Pietre E.
YU, Jimmy Y.
BRADLEY, Diana L.
BRATCHEN, Shawn R.
CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 70.3%;
al Similarity 90.3%;
502; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Incyte ID
HILLMAN, Jennifer
                       JONES, Anissa L.
LIU, Tommy F.
ROSEBERRY, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure;
LOCATION: 120, 765;
COTHER INFORMATION: a,
US-10-220-120-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PI
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APPLICANT:
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Matches 50
                                                                                                                                                                                                                                                                            APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAATTGAAACTGTAAAACTACAAATGGTTCATCAAATGGAGCCCCAGATGCAGTCCATGA 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 GCCTAGCTGGGAAGGTGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 AGCCAATCATCTATTGCCTGAGAGCACAGCGGAGGGACAAGGATCGGGATATAAACCCA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 CCCGACCAATCAGAGGGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAAT 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1202 CAGGAAGCAGTTAGAGCAGTCATCGGCCAACCTCCCCCAATAGCACTTGGGTTTTCCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAAGATCCACCGTGGACCCCTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGAAGGCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAG
                                                                                                                                                                                                                                                                                                                                                                                              GAATCAAAACTGTAAAACTACAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRGANISM: Homo sapiens
FRATURE:
NAME/KEY: misc_feature
CTHER INFORMATION: Incyte ID No. US20030124569A1 LI:813218.1:2000FEB01
FRATURE:
NAME/KEY: unsure
LOCATION: 307, 317-318, 335, 918, 921, 943, 1011
COTHER INFORMATION: a, t, c, g, or other
US-10-204-887-10
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                     Length 1564;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                            Score 449; DB 15;
Pred. No. 4.2e-129;
0; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/10220120 Publication No. US20040048253A1 GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PANZER, SCOTT R.
SPIRO, Peter A.
BANVILLE, Steven C.
SHAH, Purvi
CHALUP, Michael S.
CHANG, Simon C.
                                                                                                                                                                                                                                                                               Ouery Match 70.7%;
Best Local Similarity 90.9%;
Matches 490; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -10-220-120-17
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106
                                                          107 TCCACCGTGGACCCCTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAG 166
                                                                                                                                                                                                                                           GGGGACTGAGAGACTAGCTGGATTTCCTAGGCCAAGAAGATCCCTAAGCCTAG 346
                                                                                                                                                                                                  61
                                                                           2 AAGCTGTAAAACTACTAATTGTTCTTCAAAAGGAGCCCCCAGATGCAGTCCATGACTAAGA
                                                                                                                      GCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAA
                                                                                                                                      122 GCACTCC-CCCAAGGAAATTTCAACTGCACAACCCCTACTACAACCCCCAATTCAGCAGGAA
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CHEN, Alice D'SA, Steven A. AMSHEY, Stefan DAHL, Christopher R. DANIELS, Susan E. DUFOUR, Gerard E.

FLORES, Vincent FONG, Willy T. GREENAWALT, Lila B.

APPLICANT: APPLICANT: APPLICANT:

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1026 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCGAAGCTGTAAAACTA 1085
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                                                                                                                                              6949 GCATTCCAGTTGGGCAACTGCTACCTCTTTGGGTCCCCCTTTGTATGGAAGCTCTGT 7008
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                                                                          -----AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAG 462
                                                                                                                                                                                                521
                                                                                                                                                                                                                                                                   581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CTGGACCGGCCTGCTAGCCCCATGCTCAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                              CCAATCATC-TATTGCCTGAGAGCACAGGGGGGGACAAGGATGGGGATATAAACCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTA
GCATTCGAGCCGGCAACGCCACTTTGGGTCCCCTTTGTATGGCCGCTCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REPERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
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Pred. No. 9.7e-122;
0; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 718, Application US/10322281; Publication No. US20040126762A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , LOCATION: (1) ... (44063)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.3%;
86.1%;
                                                             353 AGGIGACIGCAI-CCACCI
                                                                                                                                                                                                                                                                                                                                                                        7009 TITCACTCIAIT 7020
                                                                                                                                                                                                                                                                                                                                              582 TITCACTCTAIT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 86.1
Matches 556, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 34
US-10-322-281-718
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                                                                                                                                                                                                                                                                            522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                               577
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                                                                               301 CIGGAAGGIGACCGCGICIACCITIAAACACGGGGCIIGCAACTIAGCICACACCCAAC 360
                                                                                                                        457
                                                                                                                                                       420
                                                                                                                                                                                          517
           GGGGACTGAGAGAGAGTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9936, Application US/10198846

Sequence 9936, Application US/2003009974A1

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: AL, Yongyao
APPLICANT: AL, Yongyao
APPLICANT: AL, Yongyao
APPLICANT: AL, Yongyao
APPLICANT: MINENTION: Rathlen
APPLICANT: Steinmann Kathlen
APPLICANT: THE OF INVENTION: PREVENTION AND TITLE OF INVENTION: PREVENTION AND TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REPERENCE: MRI-049
CURRENT PELLORION NUMBER: 60/306,220
PRIOR FILLING DATE: 2002-07-18
PRIOR FILLING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOSTWARE FEALEST OF WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6409 CCCTGTATCTTTAACCTCCTTGTTAAGTTTTGTCTTCCAGAATCAAAGCTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGAC-TAAGATCCACGTGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTGGACCGGCCTGCTAGCCCCATGCTCGATGACATTGAAGGCACCCCTCCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGG
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                                                                                                                                       AATAGCCAATCATCTATTGCCTGAGAGCACAGGGAGGACAAGGATCGGGATATAAAC
                                                                                                                                                                                                                                                                                   1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                      407 CAATC-----AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGA
                                                                                                                                                                                                                                                               CCAGGCATTCGAGCCGGCAACGGCAACCCCCTTTGGGTCCCCTTTGTATGGGCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 434.4; DB 14; Length 7974;
Pred. No. 3.3e-124;
0; Mismatches 56; Indels 19;
                                                                                                                                                                                                                                                                                                                                                         CTGTTTTCACTCTATT 593
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Best Local Similarity 87.7%;
Matches 537; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-198-846-9936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 9936
LENGTH: 7974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422 AGCCAGCAATRGCTACCCTCTATGGATCCCCTCCCTTTGTATGGGAGCTCTGTCTTCACT 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                     302 ATAAGAGAGCTTACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATC
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827 129
CURRENT FILING DATE: 2002-04-30
FRIOR PILING DATE: 2002-04-30
FRIOR PILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-07-20
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-02-24
FRIOR FILING DATE: 2000-02-24
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FRIOR FILING DATE: 1999-09-28
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FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-08-08
FRIOR FILING DATE: 1999-09-08-08
FRIOR FILING DATE: 1999-08-08-08
FRIOR FILING DATE: 1999-08-08-08
FRIOR FILING DATE: 1999-08-08-08
FRIOR FILING DATE: 1999-08-08-08
FRIOR FILING DATE: 1999-08-08-08
FRIOR FILING DATE: FARESQ for Windows Version 4.0
FRIOR FILING DATE: FARESQ for Windows Version 4.0
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                                                                                                                                                              242 GGGAAGTGACTGCATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACGCCCGACCA
                                                                                                                                                                                                                                                                         ATCAGAGAGCTCACTAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATC
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182 GGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACTAAGATCCCTAAGCTAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                            ATCTATTGCCTGAGGCACAGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCG
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93.4%; Pred. No. 1.1e-121;
ive 1; Mismatches 30;
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US-10-027-632-289680
; Sequence 289680, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
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; ORGANISM: Human
US-10-027-632-289680
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Matches 453;
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                   1312 AGGACTAACTGGATTTCCTAGGCCAACTAAGAATTCCCAAGCCTAGCTGGGAAAGGTGAC 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTAGAGCGGTCA-TCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGGGGG 288
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                                                                                                                                                              1372 TGCACCCACCTTTAGACATGGGGCTTGTAACTCAGGTCACACCCGACCAATCAGGCAGTA
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CURRENT PELING DATE: 2002-04-30
RIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-24
PRIOR PAPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-4
PRIOR PILING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE FAILNG DATE: 1999-08-09
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                                                                                                                                                                                                                                                     412 - AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAG-CCAATCA
                                                                                                                                                                                                                                                                                                                                                                                                        TCTATTGCCTGAGAGCACAGGGGGGGGACAAGGATCGGGGATATAAACCCCAGGCATTCGA
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Pred. No. 1.1e-121;
1; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 289680, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.4%;
Matches 453; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-027-632-289680
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APPLICAMY: INFORMATION, Stephen B: ALICAS, Christina M;
APPLICAMY: INFORMATION, Stephen B: ALICAS, Christina M;
APPLICAMY: DINCOLM, Stephen B: ALICAS, Chanifer L.;
APPLICAMY: DINCOLM, Stephen B: ALICAS, Chanifer L.;
APPLICAMY: FLORES, Vincent Z.; DAFFO, Abe;
APPLICAMY: FLORES, Vincent Z.; DAFFO, Abe;
APPLICAMY: PLORES, Vincent Z.; DAFFO, Abe;
APPLICAMY: PERALTA, Careyna H.; DAVID, Marie H.;
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: LEWIS, Samantha A.
APPLICAMY: MARRER: US 001-01-15
CURRENT APPLICATION NUMBER: US 60/261,865
PRIOR FILING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/263,329
PRIOR APPLICATION NUMBER: US 60/263,329
PRIOR APPLICATION NUMBER: US 60/263,131
PRIOR APPLICATION NUMBER: US 60/263,039
PRIOR APPLICATION NUMBER: US 60/263,106
PRIOR APPLICATION NUMBER: US 60/263,106
PRIOR PLING DATE: 2001-01-19
PRIOR PLING DATE: 2001-01-19
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PRIOR PLING 
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OTHER INFORMATION: Incyte ID No: LI:1147914.1:2001JAN12
                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: 484
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 47, Application US/10466531; Publication No. US20040166500A1; GENERAL INFORMATION:
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Sublication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION:
MYCARDIAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 17699
LENGTH: 50353
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                                                                                                   349 GGGAAGGTGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCA
                                                                                                                            242 GGGAAGGTGATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACGCCGACCA
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                                       182 GGACTGAGAGACAGAGCTGGCTGGATTTCCTAGGCCAACTAAGAATCCCTAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.99
Matches 535; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-741-600-17699
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                                                                                                                                                                                 7;
                                                                                                                                             548;
EXPRESSED IN BONE MARROW, SIGNAL = 1.4
EST HUMAN HIT: B1087886.1, EVALUE 1.00e-122
EST-HUMAN HIT: B1087886.1, EVALUE 1.00e-122
SWISSPROT HIT: P03384, EVALUE 2.00e-01
NT HIT: AL163280.2, EVALUE 0.00e+00
                                                                                                                                             Length
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                                                                                                                                                                                     Indels
                                                                                                                                           62.3%; Score 395.8; DB 16;
.larity 89.5%; Pred. No. 1.1e-112;
Conservative 0; Mismatches 47;
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APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC003C1
CURRENT APPLICATION NUMBER: US/10/242,355
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,897
PRIOR FILING DATE: 2001-01-17
PRIOR PLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
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PRIOR PRILING DATE: 2000-06-38
PRIOR PRILING DATE: 2000-06-38
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PRIOR PRILING DATE: 2000-06-38
PRIOR PRILING DATE: 2000-06-38
PRIOR PRILING DATE: 2000-06-31
PRIOR PRILING DATE: 2000-08-41
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR PRILING DATE: 2000-08-41
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
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    ) OTHER INFORMATION: E.
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; OTHER INFORMATION: E.
; OTHER INFORMATION: N.
US-10-029-386-8554
                                                                                                                                                                    Best Local Similarity
Matches 461; Conser
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US-10-242-355-1175/c
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: HAnzel, David R.
APPLICANT: HANZEL, David R.
APPLICANT: HONGINGHE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REPERBNUE: ADMICA-X-2 CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                  1038
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                                                                                                                                                                                                              AC-TANGATICCACCGTGGACCC-CTGGACCGGCCTGCTAGCCCCATGCTCAATG
                                                                                                                                                                                                                                                 ACATTGAAGGCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTATGCCCCAATT
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                                                                                           Gaps
                                                  Length 1394;
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OTHER INFORMATION: EXPRESSED IN HEAR, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN FRAIN, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN FIAL LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.6
                                                  5; DB 18;
1.1e-118;
                                                    Score 415.6;
Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8554, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
                                                    65.4%;
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                               Query Match
Best Local Similarity
Matches 532; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 39
US-10-029-386-8554/c
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                  US-10-466-531-47
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                                                                                                                                                                      Query Match 61.2%; Score 388.4; DB 17; Length 23855; Best Local Similarity 83.1%; Pred. No. 1.3e-109; Matches 552; Conservative 0; Mismatches 71; Indels 41; Gaps
                                                            - See File Wrapper or PALM
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - 8
NUMBER OF SEQ ID NOS: 1267
SEQ ID NO 1175
LENGTH: 23855
                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-10-242-355-1175
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000000000000000000000000000000000000000		RESULT 1 BC030968 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE ATTHORS	AUTHORS  TITLE JOURNAL MEDIJINE PUBLINE PUBLE AUTHORS TITLE JOURNAL REMARK COMMENT
			predicted by chance to have a score of the result being printed, otal score distribution.  RIES  Description  EC030968 Home sapi CR672148 full-leng CR67217248 full-leng CR622175 full-leng CR622175 full-leng CR622175 full-leng CR622175 full-leng CR622175 full-leng CR622175 full-leng CR622175 full-leng CR622175 full-leng CR622175 full-leng BX33769 BX337769 BX33769 BX337769 BX33769 BX337769 BX33769 BX37769 CR6211669-Ren_trogl AQ121669-Ren_trogl AQ121669-Ren_trogl AQ121663-Ren_trogl AQ121663-Ren_trogl AQ121663-Ren_trogl AQ121663-Ren_trogl AQ121663-Ren_trogl AQ121663-Ren_trogl AQ121663-Ren_trogl AQ121663-Ren_trogl AQ121663-Ren_trogl
GenCore version 5.  Copyright (c) 1993 - 2005 C cleic - nucleic search, using sw model n: February 21, 2005, 06:52:54; [wi] 122 ct score: 635 nce: 1 ccctgtatctttaacctcct ng table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 hed: 34239544 seqs, 19032134700 res	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries EST:* 2: 9D est2:* 3: 9D htc:* 4: 9D est2:* 5: 9D est4:* 6: 9D est5:* 7: 9D est5:* 7: 9D est5:* 9: 9D est5:* 9: 9D est5:* 9: 9D est5:* 9: 9D est5:*	**  **  **  **  **  **  **  **  **  **

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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 9100 GE EVRX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | 191 9100 GE EVRX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                                                                                                                                                                                                                                                                                                   Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 2748)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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ive 0; Mismatches 42;
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/organiam="Homo sapiens"
/mol type="mRNN"
/db_xref="taxon:9606"
/clone="CSOBOLL2Y124"
/tissue type="placenta"
/plasmid="pcMVSPORT_6"
                                                                                                                                              Homo sapiens (human)
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   cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTAAACATGGGGCTTGCAACTTAGCTCACACCGACCAATCAGAGGCTCACTAAAATG
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larity 92.6%; Pred. No. 3.6e-133;
Conservative 0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4724433"
/tissue_type="Placenta"
/clone_lib="NIH MGC_79"
/lab_host="DH10B"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I. (Dases I to 2500)
Li, W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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                                     1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                                                                                                                                                                       ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATGTATTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                           361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
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Pred. No. 5.7e-130;
0; Mismatches 40; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACCCCTTTGGGTCCCCTTCCTTTGTATGGGCGCTCTGTTTTCACTCT 590
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="teaxon:9606"
/clone="CSODIOS1YM13"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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1. .2500
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HTC; CNSLT_CDNA.
Homo sapiens (human)
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Best Local Similarity 91.1%;
Matches 534; Conservative (
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2 (bases 1 to 2500)
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Direct Submission
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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full-length cDNA clone CS0DI022YJ18 of Placenta Cot 25-normalized chit. Hand in the cot 25-normalized cot 100 community of the contract cot 25-normalized cot 100 community contract cot 25-normalized cot 100 community contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract contract co
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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                                                 1 CCCIGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
       AGAGCACAGGGGAGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Pred. No. 3.4e-130;
0; Mismatches 42;
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/db_xref="taxon:966"
/dlone="cS0D1022v118"
/tissue_type="Placenta Cc/plassue_type="Placenta Cc/plassue_type="placenta"
/plassuid="pcMVSPORT_6"
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2748 bp mRNA linear HTC 21-JUL-2004 of Full-length cDNA clone CS0DI044YK06 of Placenta Cot 25-normalized CR625046
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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                                                                                       1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
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                                                        15;
                         Length
                                                        Indels
                    Score 485.6; DB 4;
Pred. No. 2.2e-129;
0; Mismatches 49;
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HTC; CNSLT_CDNA.
Homo sapiens (human)
Homo sapiens
                       76.5%;
ilarity 89.9%;
Conservative 0
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Genoscope.
Direct Submission
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                                          Best Local Similarity
Matches 570; Conserv
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| organism="Homo sapiens" |
| organism="Homo sapiens" |
| db xref="taxon:966" |
| db xref="taxon:966" |
| clone="INAGE:493894" |
| clone="MCG36" |
| lab Fost="MCG36" |
| lab Fost="DH10B" |
| note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."
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602852690F1 NIH_MGC_10 Homo Bapiens cDNA clone IMAGE:4993894 5',
mRNA sequence.
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NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapberr@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIO15 row: d column: 23
High quality sequence stop: 762.
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CTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
               2033 CTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAAAGGCACCCCTCCTGAG
                                                               GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGT
                                                                              2093 GAAATCTCAGCTGCACAACCTCTACTACGCCCCAATTCAGCAGAAGCAGTTAGAGCGGT
                                                                                                                                241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAGAC
                                                                                                                                                                                               AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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Homo sapiens (human)
Homo sapiens
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/tissue type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7" /clone lib="GRN PRENEU" /note="oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
                                                                                    that
                             L (Dases I to 'Naj', Yeik, Guegler, K., Rao, M.S., Murage, J., Fisk, G.J., Brandenberger, R., Wai, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L. W.

Leabkowski, J and Stanton, L. W.

Leabkowski, J and Stanton, L. W.

Lontoriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Lontoriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Control burdenberger R

Regenerative Medicine

Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 760

Email: rbrandenberger@geron.com

Insert Length: 719 Std Error: 0.00.
                                  ., Fisk, G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435 TAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGAGCACAGGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCCCTGGACCGGCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              547 TAGGCAAAGACAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGAGCACAGCAGGA
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                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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17000600005410 GRN_PRENEU Homo sapiens CDNA 5', mRNA sequence...
CN272394
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                                                                                                                                                                                                                                                                                                                                                              40; Indels
                                                                                                                                                                                                                                                                                                                         Score 485; DB 3; L
Pred. No. 4.3e-129;
0; Mismatches 40;
                                                                                                                                                                                /organism="Homo sapiens"
mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO44YK06"
/tissue_type="Placenta Cot
/plasmid="pcMVSPORT_6"
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nilarity 91.1%; I
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecof V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                      758 bp mRNA linear EST 08-APR-2004
BX357208 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI022VJ18 3-PRIME, mRNA sequence.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="ist strand cDNA was primed with a Not!-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                        481 AGAGCACAGGGGGGAGGAACGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                       <u>ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTG</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.5%; Score 466.6; DB 5;
88.8%; Pred. No. 7.1e-124;
iive 9; Mismatches 43;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI022XJ18"
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1 (bases 1 to 1071)

2 Li,W.B. Gruber,C., Jessee,J. and Polayes,D.

Rull.length cDNA libraries and normalization

1 (npublished (2001)

2 Rull.length cDNA libraries and normalization

Contact: Genoscope

Contact: Genoscope

Contact: Genoscope

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Ist strand cDNA was primed with a NotI-oligo(dT) primer: Five prime end enriched, double-strand cDNA was digested with Not I and Cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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1071 bp mRNA linear EST 08-APR-200-
X3455666 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
Clone CSODIO46YA18 3-PRIME, mRNA sequence.
BX365066
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1046YA18"
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Submitted (20-JUJ-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dI) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Li W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length, CDNA libraries and normalization
                                                                                                                                                                                                                                                                                                               CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTTCCTGTTGAGAGGGGGACTGAGAGAC
                                                                     CGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAAC
                                                                                                            301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
                                                                                                                                                                      GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGGTC
                                                                                                                                                                                                      228 ACATCCACCITIAAACACGGGGCTIGCAACTIAGCICACACCTGACCAATCAGAGAGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.2%; Score 464.6; DB 3; Length 2716; 90.9%; Pred. No. 3.6e-123; Live 0; Mismatches 39; Indels 12;
                                                                                                                                                                                                                                                                                                                                                           573
                                                                                                                                                                                                                                                                                                                                                                          48 CMACCCCCYCTGGGTCCCCTCCCTTTGTATGGG 16
                                                                                                                                                                                                                                                                                                                                                           CAACCCCTTTGGGTCCCCTCCCTTTGTATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODE013Y120"
/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR613169.1 GI:50493976
HTC; CNSLT_CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTC; CNSLT_cDNA.
Homo sapiens (human)
Homo sapiens
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2 (bases 1 to 2716)
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Best Local Similarity 90.99
Matches 510; Conservative
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                                                                                                                                                       CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCC
                                                                                                                                                                                                                                                  ------caaarccaacccaacarccaacacraacacraacarcracccacacac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC
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GSS 04-NOV-2001
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRX cedex - FRANCE
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
last strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCRWSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="CSODIO18YH07"
/tissue type="PLACENYTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lib="strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Pred. No. 4.5e-120;
1; Mismatches 63;
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/mol_type="mRNA"
/db xref="taxon:9606"
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87.0%;
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BX378303 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
CLONE CSODI018YH07 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACATCCACCTTTAAACACGGGGCTTGCAACTTRGCTCACACCTGACCAATCAGAGGCT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACTAAAATGCTAATTAGGCAAAGACAGGAGGTAAAGAAATAGCCAATCATCTATTGCCT 112
                                                                                                                                       sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                               CIGGACCGGCCIGCIAGCCCAIGCICCGAIGITAAIGACAIIGAA-GGCACCCCICCCGA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
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1 (Dases 1 to 1058)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

W.B., Gruber, C., Jessee, J. and normalization
Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30439129.
                                                                                                                                                                                                                                                                  9
         /db_xref="taxon:9606"
/clone="CSODIOSIYN13"
/tissue type="PLACENTA COT 25-NORWALIZED"
/clone="PLACENTA COT 25-NORWALIZED"
/clone="Lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="lst strand cDNA was primed with a Not!-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not! I and cloned into the Not! I and ECOR V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTAGCTGGGAAGGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGAGCACAGGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGG
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                                                                                                                                                                                                                                                                                                                                                                 CACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCT
                                                                                                                                                                                                                                                                  CCTTGTTAAGTTTGTCTTCCAGAATCAAAACTGTAAAACTA
                                                                                                                                                                                                                                                                                                        CCCTGTATCTTTAACCTCCTTGTTTAACTTTGTCTTCCAGAATCGAAGCTGTAAAACTA
                                                                                                                                                                                                                                                                                                                                         CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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                                                                                                                                                                                            988;
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                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                            47;
                                                                                                                                                                                            5;
                                                                                                                                                                                        Score 454.2; DB E
Pred. No. 3e-120;
2; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BX378303.2 GI:46557492
                                                                                                                                                                                          71.5%;
larity 89.1%;
Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                                                                                                                           Local Similarity
wes 525; Conserv
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National Cancer institute, Cancer Serious Fincers, Cancer Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CNA Calone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1645 Std Error: 0.00
Seg prime: -40m13 fwd. ET from Amersham
High quality sequence stopp: 475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab.mstz=npHlOB"
/clone lib="Soares testis NHT"
/clone lib="Soares testis NHT"
/note="Vector: pTyT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                             AA781423 494 bp mRNA linear EST 31-DEC-1998 aj26c03.81 Soares testis NHT Homo sapiens cDNA clone 1391428 3' similar to contains PTR7.tl PTR7 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAGGAAATCTCAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 padadogicicacipaparicciparifaddicababacaddagafahagaaafadccaafaaf 187
                                                                                                         186 TTATTGCCTGAGAGTACAGCGGAAGGACAATGATCGGGATATAAACTCATGCATTCGAG 127
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                     471 CTATTGCCTGAGAGCACAGGGGAGGACAAGGATCGGGATATAAACCCCAGGCATTCGAG
           -AGAGAGCTCACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAAAATAGCCAATCAT
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                                                                                                                                                              531 CCGGCAACGCCCCTTTGGGTCCCCTCTTGTATGGG 573
                                                                                                                                                                                                    84
                                                                                                                                                                                  126 CCACCAATGGCTACCCTTTTGGGTCCCCTCCTTTGTTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 437; DB 1; L
Pred. No. 2.5e-115;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1391428"
                                                                                                                                                                                                                                                                                                                                                                                              AA781423.1 GI:2840754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.8%;
llarity 92.7%;
Conservative
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Best Local
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AA781423/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGACTATCTGGATTTCCTAGGCCAACTAAGAATCCCTAAGCCTAGGGAAGGTGAC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACATTCACTTTTAAACACAGGGCTTGCAACTTAGCTCACACCCGACGAATCAGGTAGTA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 666 CCNTGGATCTTTAACGTCCTTGTTAAGCTTGTCTTCCAGAATCGAAGCTGTAAAACCA 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACGATTGAAGGCACCCCTCCCGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAATCTCAACTGCAC-AACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGG 239
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 troglodytes DNA, clone: PTB-130M15.F, genomic survey sequence
                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Gaps
                                                                                                                                                                  Fuliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 450.8; DB 9;
Pred. No. 2.7e-119;
0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .689
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon.959"
/clone="PTB-130M15.P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                       Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : pKS145
   AG121669.1 GI:16650834 GASS.
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88.3%;
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515; Conservative
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R.Site 1
R.Site 2
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522 bp mRNA linear EST 01-JUN-2000
EST383642 MAGE resequences, MAGL Homo sapiens CDNA, mRNA sequence.
double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCATCCACCTCTAAACATGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGAGCTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 ACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTGACCAATCAGAGGCTK 172
                                                                                                                                                                                                                                                                                                                                                                                                                        AGGACTAGGTGGATTTCCTAGGCCAACGAGAATCCCTAAGCCTAGCTGGGAAGGTGACT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGACCCGCCTGCTAGCCCCATGCTCGATGATGACATTGAAGGCACCCCTCCCGAG 180
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases I to 522)

Hegde, P., Oi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I. E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackehbush
The Institute for Genomic Research
The Institute for Genomic Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGCACAGCGGGACAAGGATCGGGATATAAACCCCAGGCATTCGAGCCGGCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTCTTCCAGAATCGAAGCTGTAAAACTA
                                                                                                                                                                                          CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
                                                                                                                                                                                                                                                                  CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
                                                                                                                                  1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATCAAAACTAAAACTA
                                                                                                                                                                                                                                                                                                        GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGAAAGCAGTTAGAGCGGT
                                                                                                        13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541 CAACCCCTTTGGGTCCCCTTCTTGTAIGGGCGCTCTGTTTCACTCTAT 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1019;
                                                                                                        Indels
                                                                                                      99
                                                                           cch
al Similarity 83.4%; Pred. No. 1.1e-114;
494; Conservative 19; Mismatches 66;
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AW971553.1 GI:8161399
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AW971553/c
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SOURCE
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BX439636.2 GI:47000005
EST.
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                                                                                                                                                                                                                                                                           TGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATTTCACTCTATTAAATCTT 610
                                                                                                                                                                         255
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/clone="CSODEO12YJ34"
/clone="CSODEO12YJ34"
/clone="Tabe"Homo sapiens PLACENTA"
/none="Tabe"Homo sapiens PLACENTA"
with a NotI-oligo(dT) prImer. Five prime end enriched,
                            CTGCACAACCCCTACTATGCCCCCAATTCAGCGGGAAGCAGTTAGAGCGGTCATCAGCCAA
                                           GGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGGTGGGAAGGTGACTGCATCCACCT
                                                                                                                                                                                                   371 CTAAACATGGGGCTTGCAACTTAGCTCACCCGACCAATCAGAGAGCTCACTAAAATGC
                                                                                                                                                                                                                                                           TAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGAGCACAGC
                                                                                                                                                                                                                                                                                                                   GGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGGCAACCCCTT
                                                                                                                                                                                                                                                                                                                                                                                          CCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGACAGGACTAGCT
                                                                                                     134 AGGAGGACAATGATCGGGATATAAACCCAAGTCTTCGAGCCGGCAACGGCAACGCATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          division of Invitrogen.
This sequence cluster 4215.r
Hots endemore belongs to sequence cluster, see
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE012DE12NP1&c=4215.r.
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                                    191
                                                              434
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BX439636/c
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KEYWORDS
SOURCE
ORGANISM
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480

112

540

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/gex="male"
/cell type="mononuclear lymphocyte"
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/lab_host="E. Coli SOLR"
/clone_lib="Katze_MMSP"
/note="Organ: spleen; Vector: Uni-ZAP XR; Site_1: EcoR I;
Site_2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCACCAGATGGAGTCCATGACTAAGATCCACGTGGACCCCTGGACCGGCCTGCTAGCCC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tr.--GGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTCACTCTATTTCACTCTATAAA 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 AGCACTTGGGTTTTCCTGTTGAGAGGGGGACTGAGAGACAGGACTAGCTGGATTTCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u> agcactriegartrirccretreraagegegeacreagagacageacraecregartriccra</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTTGCAACTTAGGTCACACCGACCAATC-----AGAGAGCTCACTAAAATGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 TTTTAAATTTGTTTCTTCCAGAATCGAAGCTGTAAAACTACAAATGGTTCTTCAAATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 ATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAGGAAATCTCAACTGCACAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 CCTACTACGCCTCAGTTCAGCAGAAGAGTAAGAGCAGTCATCAGCAACTCCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 430.2; DB 7; Length 870;
Pred. No. 2.6e-113;
0; Mismatches 88; Indels 14;
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.02.24. 676 Q20 bases.
PCR PRimers
FORWARD: CCCTCACTAAAGGGAATAGGTAA
BACKWARD: CACTAATAGGGAATTGGGTA
Insert Length: 870 Std Brror: 0.00
Plate: CL000135 row: H column: 02
Seg primer: CCCTCACTAAAGGGAACAAAA
       USA
                                                                                                                                                                                                                                                /organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9544"
/clone="IBIUW:10227"
                                                                                                                                                                                                               Location/Qualifiers
1. .870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.7%;
llarity 83.8%;
Conservative (
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527; Conserv
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Best Local S
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CN645411
CN645411.1 GI:47158854
EST.
                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                     97 ATGACTAAGATCCACCGTGGACCCCT-GGACCGGCCTGCTAGCCCATGCTCCGATGTTAA 155
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                                                                                                                                                                                                                                                                                                                                                                                                                               274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCACACCCGACCAATCAGAGGCTCACTAAATGCTAATTAGGCAAAAATAGGAGGTAA 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Cercopithecidae, Macaca.

(ercopithecidae, Macaca.

1 (bases 1, Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L. (Large-scale Rhesus Macaque cDNA Sequencing Unpublished (2003)

Contact: C. Magness
Illumigen Biosciences Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 GTTCAGCAGGAAGCAGTTAGAGTGGTCATCAGCCAACCTCACCAACAGCACTTGGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 TGACATTGAAGGCACCCCTCCCGAGGAAA-TCTCAACTGCACAACCCCTACTATGCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGTTGAGAGGGGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACGAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTAAGCCTAGCTGGGAAGGTGACTGCATCCACCTCTAAACATGGGGCTTGCAACTTAG
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                                                                                                                                                                                                                                                                                                              215 ATTCAGCGGGAAGCAGTTAGAGCGGTCATCAGCCAACCTCCCCAACAGCACTTGGGTTTT
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                       5,
                                                                                                                                                                                                                       Length 522;
                                                                                                                                                                                                                                                       Indels
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                                                            Location/Qualifiers
1.522
/ Caganism="Homo sapiens"
/mol_type="mRNA" serion 1.546"
/db_type="mRNA" serion 1.566"
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/db_type="maxon:9660"
                                                                                                                                                                                                                     Score 432.4; DB 2;
Pred. No. 5.5e-114;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta (rhesus monkey)
                                                                                                                                                                                                                     68.1%;
91.8%;
              Email: johng@tigr.org
Plate: 292
                                              Seg primer: Forward.
                                                                                                                                                                                                                       Query Match 68.1
Best Local Similarity 91.8
Matches 479; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca mulatta
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CN645411
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DEFINITION
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Eujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Toyoda, A., Taylor, T.D., Yada, T., Toyoda, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Toyoda, Y., Matanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:is1-45-503-9117)
Tel:is205-9111, Fax:81-45-503-9170)
Tel:is304-9170, Fax:81-45-503-9170)
Tel:is304-9170, Fax:81-45-503-9170)
Tel:is304-9170, Fax:81-45-503-9170, Mail Sac Fixen.go.jp/, Was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1386 CGAGCTGGGAGTGGCCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTC 1445
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Pan troglodytes DNA, clone: PTB-008021.F, genomic survey sequence.
AG033781
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bu troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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241 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC
                                                                                                                     301 AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCT-GGGAAGGTGAC
                                                                                                                                                                                                                                                                                                                                                                ---AGAGAGCTCACTAAAATGCTAATTAGGC-AAAAATAGGAGGTAAAGAAATAGCCAAT
                                                                                                                                                                                                                                          360 TGCATCCACCTCTAAACATGGGGC--TTGCAACTTAGCTCACACGACCAATC----
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BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="lymphoblast"
/clone_lib="PTB_Chimpanzee_Male_BAC_Library"
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-008021.F"
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R.Site 2 : SacI.
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Contact: MGC help desk
Email: cgapber-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Meb Site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plates 37 Row: m Column: 12 This clone has the following problem: retained intron. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTC 04-MAR-2003
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Primates, Catarrhini, Hominidae, Homo.
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Submitted (02-APR-2002) National Institutes of Health, Mammalian
Submitted (02-APR-2002) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Pred. No. 1.9e-111;
0; Mismatches 75; Indels 18
                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                 Homo sapiens, clone IMAGE:4770655, mRNA.
BC026287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="INAGE:4770655"
/tissue type="Placenta"
/clone="libe"NIH MGC 79"
/lab host="blub"
/note="Vector: pDNR-LIB"
                                                                                                        766 GCTCAAAAAAACATATTAAAAAATAAAA 794
                                                     607 TCTTGCAACTGAAAAAAAAAAAAAA
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Best Local Similarity 85.7%;
Matches 557; Conservative
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Mammalia; Eutheria; 1
1 (bases 1 to 1500)
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
Homo sapiens
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8 셤 ò g ò 유 ò 셤 ઠે g ò g ઠે g ઠે 8 ઠે 셤 ò 용

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/tissue type="anaplastic oligodendroglioma"
/lab_host="DH108"
/lab_host="DH108"
/clone llb="WOT GGAP_BRN25"
/note="Organ: Drain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st modified polylinker; Site_1: Not I: oligo(dT) primer [5' strand cDNA was primed with a Not I - oligo(dT) primer [5' strand cDNA was primed cDNA was ligated to Eco RI I 31; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
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Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1407 Std Brror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 455
POLXA=NO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.5%; Score 415.8; DB 1; Length 490;
larity 92.9%; Pred. No. 3.5e-109;
Conservative 0; Mismatches 33; Indels 0
                                                                                                                                               1. .490
/organism≃"Homo sapiens"
                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2167578"
                                                                                                                              Location/Qualifiers
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BE732673
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Best Local Similarity
Matches 435; Conserv
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGTTTCTTTAACCCCCGTTGTTAAGTGTGTCTCTNCCAGAATCANAGCTGTAAAGCTA
                                                                                                                                                                                                                                           CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
                                                                                                                                                                                                                                                               GAAATCTCAACTGCACAACCCCTACTATGCCCCAATTCAGCGGGAAGCAGTTAGAGCGGT
                                                                                                                                                                                                                                                                                                                                                  475 AAAATCTCAACTGCACAACCCCTACTACACCCCAGTTCAGCAGGAAGCAGTTAGAGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 ACATCCACCTTTAAACATGGGGCTTGCAACTTAGCTCACCCAACCAGTAAGGAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACTAAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATTGCCT
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                                                                                                                                                                                                       CAAATGGTTCTTCAAATGGAGCCCCAAATTG-------CAGTCCATGGACCC
                                                                                                 CCTGTATCTTTAACCTCC-TTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
                                                             Gaps
                                                           18;
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                            Length 653;
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                               6
                             Score 423; DB 9;
Pred. No. 3e-111;
                                                               0; Mismatches
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EST.
                             66.6%;
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Homo sapiens
                             Query Match
Best Local Similarity 88.03
Matches 511; Conservative
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COMMENT
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/done libe="Databox" / done libe="Databox" / done libe="Databox | / done libe="Databox | / done libe="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; / Ancee="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; / Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library wit (Life Technologies). CDNA made by oligo-dT prining. Size-selected by column fractionation; average insert size 1.08 kb Library was amplified once on solid support and plasmid DNA from library was prepared. Interpretain DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 micrograms single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
                               BIS63185 543 bp mRNA linear EST 12-MAR-2002 ie57c10.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5670930 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
High quality sequence stop: 451.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                             Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 543)
                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 543)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardensas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="Islets of Langerhans"
dev_stage="Adult"
lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: dmelton@biohp.harvard.edu
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                                                                                                                                                                             BI963185.1 GI:16337590
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                                                                                                                                                                                                                                                       Homo sapiens (human)
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Best Local Similarity 88.3'
Matches 467; Conservative
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Fax: 617-495-8557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_txef="txxxon:9606"
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/clone lib="WNH MGC 21"
/clone lib="WNH MGC 21"
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   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 440)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs.remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Thoyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM752 row: j column: 01

High quality sequence stop: 440.
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Matches 413; Conservative
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Biract Submission
and Chemical Research (RIKBN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan
1-7-1: Chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGUDBY70 651 bp DNA linear GSS 02-NOV-2001
Pan troglodytes DNA, clone: PTB-046A08.R, genomic survey sequence.
AG058970
                                                                                                                        574 CCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTCTTCCAGAATCGAAGCTGTAAAACTA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGAC 300
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                           CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC
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                                                                                        CTTCCAGAATCAAAACTGTAAAACTA
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                                            13;
Length 966;
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62.2%; Score 395.2; DB 5; 79.6%; Pred. No. 3.8e-103; ive 22; Mismatches 84;
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                                                                                            1 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCT
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                           Best Local Similarity 79.6 Matches 465; Conservative
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Luc Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX380176 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA CLONE CSODIO44YK06 3-PRIME, mRNA sequence.
BX380176.2 GI:46834414
                                                                                                                   313
                                                                                                                                                           306
                                                                                                                                                                                                         373
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//mol_type="mRNA"
//db_xref="taxon:900.
//db_xref="taxon:90144YK06"
//clone="Logo = PLACENTA COT 25-NORMALIZED"
//clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
//orde="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                     TTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACTGCATCCACCTCTA
                                                                                                                                                                                                                                       AAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                     185 AAATGCTÄATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAGTCATCTATCGCCTGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACAGCGGGAGGGACAAGGATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 CACAAGGGGGGGGACAATGATCAGGATATAAACTCAGGCATTCAAGCCAGCAATGGCTAC
                              CACAACCCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGTCATCAGCCAACCT
                                                                                                                   CCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGACAGGACTAGCTGGA
                                                                                                                                                                                                                                                                                                 374 AACATGGGGCTTGCAACTTAGCTCACACCGACCAAT-----CAGAGAGCTCACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI044BF03NP1&c=4215.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCTTTGGGTCCCCTCCCTTTGTATGGGCGCTCTGTTTTCACTCTATT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCACTTTGGGTCCCCTCCCATTTTATGGGAGCTCTGTTTTCACTCTATT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 966)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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BX380176/c
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AUTHORS
TITLE
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SOURCE
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FEATURES

ORIGIN

COMMENT

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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Matanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submitssion
Burneted (10-AUG-2001) Asao Fujiyama, The Institute of Physical
Submitted (10-AUG-2001), Genomic Sciences Center (GSC);
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
(E-mail:chimpbes@ggec.riken.go.jp, UKL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:91-45-503-9111, Fax:81-45-503-9170)
Tel:atchimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACTGCATCCACCTCTAAACA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGGAGGGACGAATCGGGATATAAACCCAGGCATTCGAGCCGGCAACGGCAACCCCCT 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCATGCTCCGATGTTAATGACATTGAAGGCACCCCT-CCCGAGGAAATCTCAACTGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCCTACTATGCCCCAATTCAGCGGAAGCAGTTAGAGCGGTCATCAGCCAACCTCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               651 GACCCCGAGATCCAGTCCATGACTAAAGACTACTGTGAACCCCTGGACTGGCCTGCTAGC
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    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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                                                                               Taylor, T.D., Yada, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.9%; Score 393.2; DB 9;
88.1%; Pred. No. 1.4e-102;
ive 0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                         /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-137E19.F"
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                               Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                                                                                                                                                                    Sequencing: -21M13
                                                                                                                                                                                                                                       clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                       (bases 1 to 701)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 88.1
Matches 465; Conservative
                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes DNA, clone: PTB-137E19.F, genomic survey sequence. AG126669 AG126669.1 GI:16655834 AGS.
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                                                                                                                                                                                                                                                                                                                                                   554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 AACAGCACTTGGGTTTTCCTGTTGAGAGTGGGGACTGAGAGACAGAACTAGCTGGATTTC 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes (chimpanzee)
Pan troglodytes
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                      78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428 TGCTAATTAGGC-AAAAATAGGAGGTAAAGAAATAG-CCAATCATCTATTGCCTGAGAGC
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                                                                                                                                                                                                                                                                                                                                        TTGTTAAGTTTGTCTTCCA-GAATCAAAACTGTAAAACTACAAATTGTTCTTCAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAGGAAATCTCAACTGCACA
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                             Length 651;
                                                                                                                                                                                                 /cell_type="lymphoblast"
/clone_lib="PTB_Chimpanzee Male_BAC_Library"
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                          Score 394.8; DB 9;
Pred. No. 4.6e-103;
0; Mismatches 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .651
/organiem="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-046A08.R"
/sx="male"
                                                                                             Location/Qualifiers
                                                 : pKS145
: SacI
: SacI
                    Sequencing: M13Rev
                                                                                                                                                                                                                                                             Query Match 62.2%;
Best Local Similarity 87.6%;
Matches 503; Conservative 0
                                                    Vector
R.Site 1
R.Site 2
       PRIMERS
                                    LIBRARY
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KEYWORDS
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472 317 412 489

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429

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CONA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Clond through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1375 Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  AA837267 GGAP GCB1 Homo sapiens cDNA clone IMAGE:1369051 similar to contains PTR7.tl PTR7 repetitive element ;, mRNA
                                                                                                                                                                                                516 ACCCAGGCATTCGAGCCGGCAACGGCAACCCCCTTTGGGTCCCCTCTCTTTGTATGGGCG 575
307 ACCIGGGAAGGIGACCACTICCACCITIAAACACGGGGCTIGCAACTIAGCICACACATG 248
                                                           247 ACCANTCAGATAGTAAGGAGAGCTCACTAAAATGCTAATTAGGCAACAACAGGAGGTAAA 188
                                                                                                                 456 GAAATAGCCAATCATCTATTGCCTGAGAGCACAGGGGAGGACAAGGATCGGGATATAA 515
                                                                                                                                        187 GAAATAGCCAATCATCTGCTACCTGAAAGCACAGTGGGAGGACAATGATTGGGATATAA 128
                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bumanlai; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 443)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA837267.1 GI:2912466
                                             405 ACCAATCA------
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AA837267/c
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Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB.
BAC end sequences of Library PTB.
Upublished

2 (bases 1 to 609)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Bunitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou, Tsurumi-ku, Vokohama, Kanagawa 230-0045, Japan
(B-mail:chimpbes@ger.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
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                                                                                      GSS 03-NOV-2001
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                                                                          AG066901 609 bp DNA linear GSS 03-NOV-200:
Pan troglodytes DNA, clone: PTB-056L15.F, genomic survey sequence.
AG066901
                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        606 Agcricragaacracaarcarrcrrcaaarggagccccaaargcagrccargacraaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .609

/organism="Pan troglodytes"

/mol type="genomic DNA"

/db xref="taxon:9598"

/clone="PTB-056L15.F"

/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
                                                                                                                                                                                         Pan troglodytes (chimpanzee)
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LIBRARY
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GSS.
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All28526 Goreg placenta 8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1714147 3' similar to contains PTR7.bl PTR5 repetitive element;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I Dases 1 to 436 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                     /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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                                                                                                                                                                               Length 712;
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                                                                                                                                                                                 DB 8;
                                                                                                                                                                                 Score 387.2; DB 8;
Pred. No. 7.5e-101;
0; Mismatches 94;
                                               /mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=3131 Col=8 Row=J"
                                 organism="Homo sapiens"
Location/Qualifiers
1. .712
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                                                                                           /sex="male"
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High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Gle-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3131 row: J column: 8
Seq primer: MI3 Reverse
Class: BAC ends
High quality sequence stop: 712.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 712)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Heller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
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saplens genomic clone Plate=3131 Col=8 Row=J, genomic survey
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                                                                                                                                            CAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGGGGGACTGAGAGACAGG
                                                                                                                                                                 AAAATGCTAATTAGGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGA
                                                                                                                                                                                                                                                                                                                                          184 ATCTCAACTGCACAACCCCTACTATGCCCCCAATTCAGCGGAAGCAGTTAGAGCGGTCAT
                                                                                                                                                                                                       ACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTAAGCCTAGCTGGGAAGGTGACTGCA
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                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                    1;
                      Length 443;
                                                    Indels
                    Score 392.6; DB 1;
Pred. No. 1.8e-102;
0; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATCTTGCAACTGAAAAAAAA 627
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AQ892947.1 GI:6349137
                      61.8%;
94.1%;
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                         Query Match
Best Local Similarity 94.1
Matches 418; Conservative
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/done liber Soares NFL T GBC_S1"
/done liber Soares NFL T GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_l: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Capa http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1061 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 445.
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                                                                                                                                                                                                                                                                                                                                                                                 1. .446
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/mol_type="maxNa"
/db_xref="taxon:9606"
/clone="tMAGE:2111766"
/lab_host="DH108"
AI393478.1 GI:4223025
                                       Homo sapiens (human)
                                                              Homo sapiens
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                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 720 Std Error: 0.00.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 428.
Location/Qualifiers
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                                                                                                                                                                                                          1. .436
/organiam="Homo sapiens"
/mol_type="mRNA"
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 485)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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This clone is available royalty-free through LLML ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 470.
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                                                                                                                               386 GCAACTTAGCTCACACCCGACCAATC----AGAGAGCTCACTAAAATGCTAATTAG
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
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Totoki, Y., Watanabe, H. and Sakaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCCCCAATTCAGCGGAAGCAGTT-AGAGCGGTCATCAGCCAACCTCCCCAACAGCACT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rrrcrcrcrcagaarccaagcrgraaaacracaaarccrrcrrcaaargcagcccag 581
                                                                                                                                             641 bp DNA linear GSS 01-NOV-200
Pan troglodytes DNA, clone: PTB-012009.F, genomic survey sequence.
AG036829
AG036829.1 GI:16563702
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/organism="Pan troglodytes"
/organism="Pan troglodytes"
/mol type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-012009.F"
/cell type="lymphoblast"
/cell type="lymphoblast"
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Best Local Similarity 87.3%; Pred. No. 4.2e-100;
Matches 493; Conservative 0; Mismatches 59;
          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes (chimpanzee)
Pan troglodytes
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R.Site 1 : SacI
R.Site 2 : SacI.
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556 bp mRNA linear EST 05-AUG-2002 PLACE3 Homo sapiens cDNA clone PLACE3000382 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAGAGGGGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCCAACGAAGAATCCCTA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                              ATTGAAGGCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTATGCCCCCAATTCA
                                                                                                                                                                                                                                                                                                                             544 ATCGAAGGCACTCCTCCCGAGGAAATCTCAAATGCACAACCCCTACTATGCCCCAATTAA
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                                                                                                  40 AGAATCAAAACTGAAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATG
                                                                                                                                                                                                 ACTAAGATCCACCGTGGACCCCTGGACCGGCCTGCTAGCCCCATGCTCCGATGTTAATGAC
                                                                                                                                                                                                                                                     604 ACTAAGATCTACCGCGGATCCCTGGACCAGCCTGCTAGCCCCATGCTCGATGTTAATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                             340 AGCCTAGCT-GGGAAGGTGACTGCATCCACCTCTAAACATGGGGC--TTGCAACTTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                 220 GCGGGAAGCAGTTAGAGCGGTCATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGT
                                                   18;
  664;
  Length
                                                   Indels
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Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
59.8%; Score 379.8; DB 5; llarity 84.3%; Pred. No. 1e-98; Conservative 0; Mismatches 78;
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Unpublished (2000)
Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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       Query Match
                                 Best Local
Matches 51
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AU158595/c
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DKFZp686M05227-5', mRNA sequence.
                                                                                                                                                                                                                                                          377
                                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                          428
                                                                                                                                                                                                                                                                                                                                                                                           240 CGGGGCTTGCAACTTAGCTCACACCCAACCAATCAGATAGTAAAGAGAGCTCACTAAAAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                            488
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Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (baess 1 to 664)
Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wismann, S.
EST (Bahr, A., Lauber, J., Mewes, H.W., Weil, B., et al.)
                                                                                                                                                           317
                                                           257
                                                                                                         361
                                                                                                                                                                                                         AGCAGCACTTGGGTTTTCCTGTTGAGAGCGGGACTGAGAGACAGGACTAGCTGGATTTC 301
       CACATGCTCCGATGTTAATGACAŢCGAAGGCACCCGTCTCGAGGAAATCTCAACTGCACA 421
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Wolecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dKfz- heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp686W05227) is available at the RZPD in Berlin.
Please contact the RZPP: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GRRWANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
cDNA-collection"
                                                        ACCCTACTATGCCCCAATTCAGCGGGAAGCAGTTAGAGCGGTCATCAGCCAACCTCCCC
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JOURNAL
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ACCESSION VERSION KEYWORDS SOURCE

COMMENT

FEATURES

ORIGIN

564

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                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: Dr. Elice Spindel
Tissue Procurement: Dr. Elice Spindel
CDNA Library Preparation: CLONTECH
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3133 row: i column: 17
High quality sequence stop: 373.
High quality sequence stop: 373.
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca. I bases 1 to 862. Norl-CAAP http://www.ncbi.nlm.nih.gov/ncicgap. Norl-CAAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (
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Best Local Similarity 87.1%; Pred. No. 9.9e-96;
Matches 458; Conservative 0; Mismatches 49; Indels 19
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IMAGE:6884154 5', mRNA sequence.
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Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                            Fax: 81-438-52-3986
Enali: genomicoghri.co.jp
Enali: genomicoghri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGITAGAGCGGTCATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGGG
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59.1%; Score 375.2; DB

Best Local Similarity 84.1%; Pred. No. 2.1e-97

Matches 470; Conservative 0; Mismatches 55
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Direct Submission
Claydo-2001) Asao Fujiyama, The Institute of Physical
and Chamical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gac.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416
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                                                                                                                                                                                                                                                                                                                                   GSS 03-NOV-2001
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                                                                                                                                                                                                                                                                                                                  AGU/6758 679 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-071A23.R, genomic survey sequence.
AG076758
                                                                                                                           25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                       437 GGCAAAAATAGGAGGTAAAGAAATAGCCAATCATCTATTGCCTGAGAGCACAGGGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell type="lymphoblast"
/clone lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 364.8; DB 9; Length Pred. No. 2.3e-94; 0; Mismatches 42; Indels
                                                                                                                                                                              593
                                                                                                                                                                         /organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="PTB-071A23.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .679
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Pan troglodytes (chimpanzee)
Pan troglodytes
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R.Site 1 : SacI
R.Site 2 : SacI.
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illarity 90.3%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="DH10B"
/clone lib="Soares NhHMPu S1"
/clone lib="Soares NhHMPu S1"
/clone lib="Soares NhHMPu S1"
/clone lib="Soares NhHMPu S1"
/note="Organ: mixed (see Eelow); Vector: pT7T3D-Pac
/note="lorgan: mixed (see Eelow); Vector: pT7T3D-Pac
Site_2: Eco R1; Equal amounts of plasmid DNA_from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.B. clones 260232-265223,
340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

B. (Dases 1 to 470)
S. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
L. Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -40ml3 fwd. BT from Amersham
High quality sequence stop: 447.
Location/Qualifiers
                                                                                        A1074704 Soares NHHMPu S1 Homo sapiens cDNA clone IMAGE:1662921 3' similar to contains PTR7.t2 PTR7 repetitive element ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 470
| /organism="Homo sapiens"
| /mol_type="mRNA"
| /db_xref="taxon:9606"
| /clone="IMAGE:1662921"
| /tissue_type="Pooled human melanocyte, fetal heart, and pregnant_uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGATGTTAATGACATTGAAGGCACCCTCCCGAGGAAATCTCAACTGCACAACCCCTAC
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                                                                                                                                                                                                            AI074704.1 GI:3401348
                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
                                                                                                                                                                  sequence.
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// organism="Homo sapiens"
// mol_type="mRNA"
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// mol_type="mRNA"
// db_xref="taxon:960"
// clone="lnAson:960"
// clone="lnBase="two placentae: one from 8 weeks and another
from 9 weeks post conception"
// lab_host="DH10B (ampicillin resistant)"
// lab_host="DH10B (ampicillin resistant)"
// clone=lib="Soaree_placenta="sto9weeks_ZNbHPBtc9W"
// clone=lib="soaree_placenta="sto9weeks_ZNbHPBtc9W"
// clone=lib="soaree_placenta="sto9weeks_ZNbHPBtc9W"
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qc61e08.x1 Soares placenta 8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1714118 3' similar to contains PTR7.t1 PTR7 repetitive
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NCI-GRAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                             26
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Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infe@image.llnl.gov) for further information. Insert Length: 1184 Std Brror: 0.00
Seq primer: - 46ml3 fwd. Er from Amersham
High quality, sequence stop: 413.
Location/Qualifiers
                              295 GAAATCTCAACTGCACAACCCCTACCATGCCCCATTTCAGCAGAAGCAGGTAGAGCGGT
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                                                                                                                 element ;, mRNA sequence.
AI128496
AI128496:1 GI:3597010
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Homo sapiens
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (102-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIEM), Genomic Sciences Center (GSC);

1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL.http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the RED process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ngusuzze
Pan troglodytes DNA, clone: PTB-002120.R, genomic survey sequence.
AG030228
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                         296 CTGACTAAGAATCCCTAAGCTGGGAAGGTGACCACCACCATCCACCTTAAAACACGGGG
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BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Pan troglodytes"
/mol type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-002I20.R"
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Insert Length: 1440 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stopp: 414.
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Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Cases 1 to 425)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAI/ONAL Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BRGAP), Tumor Gen Index

Unpublished (1998)
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                                                                               CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTA
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                                       64;
  DB 9;
Score 360.6; DB 9 Pred. No. 3.9e-93, 0; Mismatches 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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  56.8%;
86.2%;
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    Query Match
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Matches 399; Conservative
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Search completed: February 21, 2005, 14:51:02 Job time : 1986.67 secs

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1 (bases 1 to 1481)
Baccala,G.P. Pradel,F.K., Bedin,F., Sodoyer,M., Ott,C., Mallet,F.,
Perron,H. and Mandrand,B.
Retroviral nucleic material and nucleotide fragments, in
particular, associated with multiple sclerosis and/or rheumatoid
arthritis, for diagnostic, prophylactic and therapeutic uses
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Perron, H., Beseme, F., Bedin, F., Paranhos-Baccala, G.,
Romurian-Pradel, F., Jolivet-Reynaud, C. and Mandrand, B.
Komurian nuclectide sequences associated with multiple sclerosis rheumatoid arthritis and a process of detecting patent: US 6582703-A 105 24-JUN-2003;
Location/Qualifiers
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    1481
    /organism="unidentified"
    /mol_type="genomic DNA"
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llarity 100.0%; Pr
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RESULT 4 AF127228 LOCUS LOCUS DEFINITION Multiple sclerosis associated retrovirus element clone CL15 env-like mRNA sequence. ACCESSION AF127228 VERSION AF127228.1 G1:5726293	KEYWORDS  KEYWORDS  Multiple sclerosis associated retrovirus element  ORGANISM Multiple sclerosis associated retrovirus element  Viruses: Retroid viruses; Retroid viruses:  REFERENCE 1 (bases 1 to 1932)  AUTHORS Komurian-Pradel, F., Paranhos-Baccala, G., Bedin, F.,  Ounanian-Paraz, A., Sodoyer, M., Ott, C., Rajoharlson, A., Garcia, E.,  Mallet, F., Mandrand, B. and Perron, H.	cia, E	Maller, F., Mandrand, B. and Perron, H.  TITLE Direct Submission JOURNAL Submitted (10-FEB-1999) UMR103 CNRS, bioMerieux, 46, allee D'Italie, Lyon 69007, France FEATURES Location/Qualifiers 1. 1932 //organism="Multiple sclerosis associated retrovirus	32" nv but interrupted by premature	codon; includes signal peptide region, and partial SU and TM regions"  misc_difference 568  /note="in clones CLI5-2 and CL37-14; results in a premature stop codon to Trp amino acid translation" /replace="a"	ORIGIN  Query Match Query Match Best Local Similarity 100.0%; Score 1481; DB 14; Length 1932; Best Local Similarity 100.0%; Pred. No. 0; Matches 1481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		OY 61 GCACCCCTCCATGCTGCTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 120	OY 121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATAGGGGTTTATCTAAGGGAAACTCC 180  Db 572 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC 631	QY 181 ACCTTCACTGCCCACACCCGTATGCCCGCAACTGCTATAACTCTGCCACTTTTGCATG 240	OY 241 CATGCAAATACTCATTATTGGACAGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT 300	Qy 301 GGAGCCACTGTTGCACTTACTTCACCCATACCAGTATGTCTGATGGGGTGGAATT 360
	541 CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTTCAATC 600	661 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTGAAACTTT 720	ATAGETCTGCCTACCCTCAGGAATATTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTG	841 AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACACCATCTAC 900 901 ACTGAACAACAATCATTATACAATCATGTGCTACCTAAGCCCCACAACAAAAGAGTACCCATT 960 901 ACTGAACAAAGAGTTTATACAATCATGTGGTACCTAAGCCCCACAAAAAAAA	961 CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGGTACTAGGCATTGGCAGTATC 1020	1021 ACACCTCTACTCTACTACAACTATCTACAAATAAATGGTGACATGGAACAG 1080 1081 GTCACTGACTCCTGGTCACCTTGCAAGATCAACTCCTAGCAGCAGTAGTCTT 1140 1081 GTCACTGACTCCTGGTCACTTGCAAGATCAACTTAACTCCTAGCAGCAGTAGTCTT 1140 1081 GTCACTGACTCCCTGGTCACTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT 1140	1141 CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA 1200 	1201 GGAGAAGACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA 1260 	1261 ATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTC 1320 	1321 CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG 1380 1321 CTCAGCCAATGGATGCCCTGGGTTCTCCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG 1380	1381 TTACTCCTCTTTGGACCCTGTALCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440 	1441 GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481 

Oy 1441 GAAGCTGTAAAGCTACAGATGGTCTTACA 	RESULT 5 AL390039/C LOCUS DEFINITION Human DNA sequence from clone R Contains ESTB, STSB and GSSB C Gene similar to NUP62 (nucleopo	VERYNORDS HTG; nucleoporin; NUP62. SOURCE Homo sapiens (human) ORGANISM Homo sapiens (constitution of the property of the prop				corresponding to the overlappin only a small overlap as describ The following abbreviations are numbers given in the feature ta	Em:, EMBL; Sw:, SWISSPROT; Tr:, on the WORMPEP database can be http://www.sanger.ac.uk/Project was generated from part of bact	chromosome X, constructed by th Group. Further information can http://www.sanger.ac.uk/HGP/Cht IMPORTANT: This sequence is not	RP13-383K5 It may be shorter be sections only once, except for The true left end of clone RP13 true left end of clone RP5-1126	This sequence has been finished as follows. An attempt is made such as compressions and repeat annotated repeat sequence eleme	ambiguous, there is an annotati RP13-383K5 is from the library of Pieter de Jong. For furthe http://www.chori.org/bacpac/hom	VECTOR: pBACe3.6. FEATURES Location/Qualifiers source 1162579	/mol_type="genomic_DNA /db_xref="taxon:9606" /chronesome="x" /man="d22.1-24"	/Clone="RP13-383K5" /Clone lib="RPCI-13.2" misc_feature complement (1232) /note="match: GSS: Em:		
AAAAACAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACAT 420 	ACAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCGGTACC 480	GITGGAIGTGCCTCCCCTGCACTTCAGGCCATACAITTCAAIC 600 	ggaacaacttcagcacagaaataaacaccacttccgtttagta 660 	GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT 720 	AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCCACACGA 780 	CAGGAATATTTTTGFCTGTGGTACCTCAGCCTATCATTGTTTG 840 	CTATGTGCTTCCTCATTCTTAGTGCCCCCTATGACCATCTAC 900 	ACTGAACAACATTTATACAATCATGTCGTACCTAAGCCCCACAACAAAAGGTACCCATT 960 	CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCACACTAGGTACTGGCATTGGCAGTATC 1020 	TCTACTACAAACTATCTCAAGAAATAAATGGTGACATGGAACAG 1080 	GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTACTCCTT 1140 	CAAAATCGAAGGTTTAGACTTGCTAACCGCCAAAGAGGGGGGAACCTGTTTATTTA	GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA 1260 	ATTCGAGATCGAATACAATGTAGAG'AGAGGAGCTTCAAAACACCGAACGCTGGGGCCTC 1320 	CCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCGCTCTAATATTG 1380 	TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440 
Oy (361 CAAGGTCAGGCAAGAGAAAAC 	421 AGCACCCTAGCCCT	Oy 541 CAAAACCCTACTAACTGTTGGF	Oy 601 CCTGTTCCTGAACAATGGAACA	Oy 661 GGACCTCTTGTTTCCAATCTGC DD 1112 GGACCTCTTGTTTCCAATCTGC	Oy 721 AGCAATACTATAGACACAACC!	Qy 781 ATAGTCTGCCTACCCTCAGGA 	Oy 841 AATGGCTCTTCAGAATCTATG'	Oy 901 ACTGAACAAGATTTATACAAT 	Oy 961 CITCCITITGITAICAGAGCA	Oy 1021 ACAACCTGTACTCAGTTCTAC'	Oy 1081 GTCACTGACTCCCTGGTCACC 	Oy 1141 CAAAATCGAAGACTTTAGAC 	Qy 1201 GGAGAAGAACCTGTTATTAT 	Oy 1261 ATTCGAGATCGAATACAATGT 	Qy 1321 CTCAGCCAATGGATGCCTGG 	Oy 1381 TTACTCCTCTTTGGACCCTGT

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an not the entire insert of clone ar because we sequence overlapping for a 100 base overlap.

RP13-383K5 is at 1 in this sequence. The 11126B12 is at 162480 in this sequence. In made according to sequence map criteria made to resolve all sequencing problems, appeats, but not necessarily within known elements. Where the sequence is reary RPCI-13.2 constructed by the group rary RPCI-13.2 constructed by the group :/home.htm
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Triph of the primary accession of the their source databases:

Triph TREMBL; Wp:, WORWPEP; Information the found at
                                                                                                                                                               pp DNA linear PRI 22-DEC-2000 RP13-383K5 on chromosome Xq22.1-24 Contains a novel gene and a novel porin 62kD), complete sequence.
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cterial clone contigs of human
the Sanger Centre Chromosome X Mapping
an be found at
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Catarrhini; Hominidae; Homo.
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s: humquery@sanger.ac.uk Clone
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m:AQ036363"
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matches 327. .356 of consensus"

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/ HOUSE - IDRAVI, TEPERAL: MRACHES GOLIS. .0322 OL COMBERGER 21897. .2288  
/ Anotes - HERRIT repeat: matches 4301. .4980 of consensus 2298. .22742. / Anotes - HERRIT repeat: matches 5623. .6135 of consensus 700tes - Alux repeat: matches 1. .306 of consensus 7049. .23286  
/ Anotes - Alux repeat: matches 5403. .5623 of consensus 700tes - LIMBS repeat: matches 5403. .5623 of consensus 70tes - LIMB repeat: matches 5006. .5082 of consensus 70tes - LIMA repeat: matches 4019. .4084 of consensus 70tes - LIMA repeat: matches 4019. .4084 of consensus 70tes - LIMA repeat: matches 4019. .4084 of consensus 70tes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - LIMA repeat: matches 70tes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes - Anotes
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/note="LIMC/D repeat: matches 5620, .5805 of consensus"
27182, .27307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9873, .21594
note="HBRV17 repeat: matches 6812, .8523 of consensus"
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//note="MIR repeat: matches 1. .89 of consensus"
25155. .26208
//note="MIR repeat: matches 144. .352 of consensus"
26155. .26697
//note="MILTIA1 repeat: matches 1. .149 of consensus"
//note="MILTIA1 repeat: matches 1. .149 of consensus"
//note="MILTIA1 repeat: matches 5939. .6162 of consensus"
//note="MILTIA1 repeat: matches 5939. .6162 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 1813 | 18319 | 1820 | 18319 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18312 | 18312 | 18312 | 18312 | 18312 | 18313 | 18312 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 | 18313 
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/hote="L1 repeat: matches 5101. .5440 of consensus"
/hote="L1M3 repeat: matches 5101. .5440 of consensus"
25437. .25742
/hote="Aluga repeat: matches 1. .307 of consensus"
25779. .25961
                                                                                                                                                            /note="12" copies 2 mer at 71% conserved"
/1010. .17166
/note="L2 repeat: matches 2688. .2750 of consensus"
/17755 .17755
/note="L2 repeat: matches 1244. .1898 of consensus"
/17839. .18106
/note="MBR70A repeat: matches 148. .418 of consensus"
/note="MBR70A repeat: matches 148. .418 of consensus"
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74306. .24593
hote="AluJo repeat: matches 1. .293 of consensus"
4594. .25109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="LTR17 repeat: matches 1. .326 of consensus"
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'note="match: GSS: Em:AQ054794 Em:AQ823559"
                                                     16067. .16294
/note="match: GSS: Em:AQ457003"
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Best Local Similarity 99.5%;
Matches 1473; Conservative
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Qy         1201         GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAGTTAAAGAA         1260           Db         20359         GGAGAAGATCGTTATTATGTTAATCAATCCAGAATTGTCACTCAGAAGTTAAAGAA         20300           Qy         1261         ATTCGAGATCGAATGTAGAGCAGAGGAGCTTCAAAACACCGGAGCGCTC         1320           Qy         1321         CTCAGCCAATGGATGCAATGTAGAGCAGAGGCTTCAAAACACCGAACACTGGGGCTC         20240           Qy         1321         CTCAGCCAATGGATGCCTGGGTTCTCCCCTTTAAGACTCTAACATATTG         1380           Db         20239         CTCAGCCAATGGATGCCTGGGTTCTCCCCTTTAAGACTCTAAGATTTG         1380           Db         20239         CTCAGCCAATGGATGCCTGGGTTCTCCCCTTTTAAGATTTGTCTTTAATATTTG         20180           Qy         1381         TTACTCCTTTTGGACCCTGGTTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATT         20120           Qy         1441         GAAGCTGTAAAGATGTTAACTCTTTAAGTTTGTCTTTCTCAGAATT         20120           Qy         1441         GAAGCTGTAAAAGATCTTAAACTCCTTGTTAAGTTTGTCTTTCCAGAATT         20120           Qy         1441         GAAGCTGTAAAAGATCTTAAAATGGAACCCA         20079	RESULT 6 CQ719381 LOCUS LOCUS LOCUS CQ719381 LOCUS Sequence 5315 from Patent W002068579. DEFINITION CQ719381 CQ719381 CQ719381 VERSION CQ719381. GG719381. G	JOURNAL Patent: WO 02068579-A 5315 06-SEP-2002; PEATURES Location (NY) (US) FEATURES Location/Qualifiers Source 12055 / Organism="Homo sapiens" / mol type="unassigned DNA" / db_xref="taxon:9606"  ORIGIN Query Match 99.0%; Score 1466.6; DB 6; Length 2055; Best Local Similarity 99.4%; Pred. No. 0; Matches 1472; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	######################################	Db 156 ACGCGCTTCCTGGAATATTGATGCCCCATCATATGGGGTTTATCTAAGGGAAACTCC 215  Qy 181 ACCTTCACTGCCCACCCCATATGCCCCCACACTGCTATAACTCTGCCACTCTTTGCATG 240  L
121   ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC   180	1 AGCACCCTAGCCCTACAAGGACTAGTTCTCTCAAAACTACATGAAACCGTCGTACC 480  1 GLILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	661 GGACCTCTTGTTTCCAATCTGGAATAACCCATACCTCAAACCTCACCTGTGTAAATT7 720  [	841 AATGGCTCTTCAGAATCTATGTGCTTCCTCATTCTTAGTGCCCCTATGACCATCTAC 20719 AATGGCTCTTCAGAATCTATGTGCTTCCTCTTAGTGCCCCCTATGACCATCTAC 900 20719 AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTAC 2060 901 ACTGAACAAGAATCATATACAATCATGTCGTACCTAAGCCCCACAACAAAAGAGTACCCATT 960 20659 ACTGAACAAGATTATAACAATCATGTCGTACCTAAGCCCCAACAAAGAAGAATACCATT 20600 961 CTTCCTTTTGTTATCAGAAGAGAGGTGCTAAGGTACTAGGTACTGGCATTGGCAGTATC 1020 20600 CTTCCTTTTGTTATCAGAAGAGAGAGAAGAATAGGCAAGAATTGGCAGTATC 20600	021 ACAACCTCTACTAGTTCTACTACAACTATCTCAAGAATAAATGGTGACTGGAACAG 539 ACAACCTCTACTCAGTTCTACTACAAACTATCTCAAGAATAAATGGTGACTGGAACAG 681 GTCACTGACTCCTGCAAGATCTACTACTACAAAATGGTGACATGGAACAG 681 GTCACTGACTCCCTGGTCACCTTGCAAGATCCAACTTAACTCCCTAGCAGCAGTAGTCCTT 679 GTCACTGACTCCCTGGTCACCTTGCAAGATCCAAAACTCCCTAGCAGCAGTAGTCCTT 671 CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTATTTTTT 671 CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTATTTTTTT 672 CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTATTTTTTTT

Oy 1441 GAAGCTGTAAAGCTACAA 	RESULT 7 BD252040 BD252040 LOCUS DEPUNITON Method for detecting	ACCESSION BD252040 TS:33061 VERSION BD252040 GT:33061 VERYWORDS JP 2002539804-AL SOURCE HOME SADIENT (Numan)		AUTHORS Perron, H. and Lafont TITLE Method for detecting JOURNAL Patent: JP 200253980 BIO MERIEUX	COMMENT OS Homo sapiens (1) PN JP 2002539804-1 PD 26-NOV-2002 PF 20-NAR-2000 JP	PR 19-MAR-1999 FR HERVE PERRON, MONIQUI PC CI2N15/09, A61R PC A61P25/00,	PC C07K14/47,C07K G01N33/15, PC FC G01N33/56.G01N33/56	(C12Q1/02, C12R1:93 A61K37/02 CC Method for det sample	FH Key FT Source FT Source FT Location/O	urce	ORIGIN Query Match Rest Local Similarity 99.28	S C	Db 1 ATGGCCTTCCTTATCA	61	121	Oy 181 ACCTTCACTGCCCACAC	Oy 241 CATGCAAATACTCATTF	Db 241 CATGCAAATACTCATTF Oy 301 GGAGCCACTGTCTTTC
361 CAAGGTCAGGGAAGAAAACAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACAT 420 	AGCA 	CATE	541 CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTTCAATC 600 	601 CCTGTTCCTGAACAACAACTTCAGCACAGAAATAAACACCACTTCGTTTTAGTA 660 	661 GGACCTCTTGTTTCCAATCTGGAAATAACCCCAACCTCAACCTCACCTGTGAAATTT 720 	721 AGCAATACTATAGACACAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACACGA 780 	781 ATAGTCTGCCTACCGTCAGGAATATTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTG 840 				1021 ACAACCTCTACTCAGTTCTACTACAAACTATCTCAAGAAATAAAT		8=8	GAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGAA	GAGATCGAATACAATGTAGGCAGAGGAGCTTCAAAACACCGAAGGGGGCCTC		1356 CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG 1415	1381 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440 
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ng superantigen activity in a biological sample.
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RS1/711,A61K38/00,A61K39/395,A61K45/00,A61K48/00,
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(3),(C12Q1/68,C12R1:93),C12N15/00,G01N27/26, PC
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/Qualifiers
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0; Mismatches
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be="genomic DNA"
i="taxon:9606"
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Oy 1441 GAAGCTGTACAGATGGTCTTACAATGGAACCCCA 1481 	8 92 TION ION N DS	SOURCE Homo saplens (numan) ORGANISM Homo saplens ORGANISM Homo saplens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REPERENCE 1 AUTHORS Lafont, M. and Perron, H. JOURNAL Patent: FR 2791140-A 1 22-SEP-2000;	BIO MERIEUX (FR)  FEATURES Location/Qualifiers  11629  /organism="Homo sapiens"  // Lype="unassigned DNA"  // Ab xref="taxon: 9606"	ORIGIN  Query Match  Query Match  Best Local Similarity 99.2%; Pred. No. 0;  Bast Local Similarity 99.2%; Pred. No. 0;  Matches 1469; Conservative 0; Mismatches 12; Indels 0; Gaps 0;	CCTTATCATACTITICCTTTACTGTTCTCTTACCCCCTTTCGCTCTC 	QY         61 GCACCCCTCCATGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 120	121 ACGCGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC 181 ACCTTCACTGCCACACCCCATATGCCCCGGAACTGCTATAACTCTGCCACTCTTGCATG	Db 181 ACTTCACTGCCCACACCCATATGCCCGCAACTGCTATAACTCTGCACTCTTTGCATG 240  Qy 241 CATGCAAATACTCATTATTGGAAAAAGATAATAATCCTAGTTGTCTGGAGACTT 300  Db 241 CATGCAAATACTCATAATTGGAAGGGAAAAAAATAATCCTAGTTGTCTGGAGGACTT 300	301	361	421	Oy 481 CATACTGGCTGGTGAGCCTATTTAATACCACCTCACGCTCCATGAGGTCTCAGGC 540	541 CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTTCAATC	Db 541 CAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCAGGCCATACATTTCAATC 600 Oy 601 CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA 660
301 GGAGCCACTGTCGTGGACTTACTTCACCCATACCAGTATGTCTGATGGGGGTGGAATT 360 361 CAAGGTCAGGCAAGAGAAAAAGTAAAGGAAGCAATCTCCCCAACTGACCCGGGGACT 420 1	421 AGCACCCTAGCCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCGGTACC 480 [	TTCAATC TTCAATC TTTAATC	601 CCHGTTCCTGAACAACGAACAACTTCAGCACAGAATAAACACCACTTCCGTTTTAGTA 660 661 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT 720 661 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACGTGTAAAATTT 720 661 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACGTGTAAAATTT 720	AGCAA       AGCAA	TGCCTACCTCAGGAATATTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTGT	941 AATGGCTCTTCAGAATCTATGTGCTTCTCTTAGTGCCCCCTTTTTTTT	61 CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTG		IAGICCII IAGICCII IAITITIA	41 CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAGAGGGGGAACCTGTTTATTATTTTA		ATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTC	1321 CTCAGCCAATGGATGCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG 1380 1321 CTCAGCCAATGGATGCCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATTT 1380	1381 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440 

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                                                                                                                                                                                                                                                                                                                                                                                /function="displaying superantigen-like properties causing polyclonal activation of human Vbeta 16 T-cells (CD3+) independent from the T-cell receptor antigen specificity" /note="surface and transmembrane regions"
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Camelo, S., Dumon, A., Jolivet-Reynaud, C., Marcel, F., Souillet, Y., Sourel, E., Gebuhrer, L., Santoro, L., Marcel, S., Seigneurin, J. M., Marche, P.N. and Lafon, M. Multiple sclerosis retrovirus particles and recombinant envelope trigger an abnormal immune response in vitro, by inducing polyclonal Vbetal6 T-lymphocyte activation Virology 287 (2), 321-332 (2001)
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Perron, H., Ounanian-Paraz, A., Marcel, F. and Souillet, Y.
Direct Submission
Submitted (21-DEC-2000) R&D, bioMerieux, Chemin de L'Orme,
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                                            Multiple sclerosis associated retrovirus element Multiple sclerosis associated retrovirus element Viruses; Retroid viruses; Retroviridae.

1 (Sess 1 to 1629)
Perron, H., Jouvin-Marche, E., Michel, M., Ounanian-Paraz, A.,
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                                                                                                                       AC023366 172918 bp DNA linear HTG 02-MAR-2000
Homo sapiens clone RP11-15N10, WORKING DRAFT SEQUENCE, 33 unordered
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172918)
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-15N10
                                                                                                                                                                                                      AC023366.2 GI:7143443
HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Bource FEATURES

		AUTHORS Rankumar, J. and Arvizu, C. TITLE Embryogenesis associated proteins JOURNAL Patent: WO 0248362-A 4 20-JUN-2002; Incyte Genomics, Inc. (US) FEATURES  Location/Qualifiers 12074 / organism="Homo sapiens" / mol Lype="unassigned DNA" . db xref="taxon:9606" / noTe="Incyte ID No: 7477736CBI"	Ouery Match 93.8%; Score 1389.8; DB 6; Length 2074; Best Local Similarity 96.2%; Pred. No. 0; Matches 1424; Conservative 0; Mismatches 57; Indels 0; Gaps 0; Oy 1 ATGGCCTCCCTTATCATACTTTTCTCTTTACTCTTTACCCCCTTTCGCTCTCACT 60 Db 64 ATGGCCCTCCCTTATTTTTTTTTTTTTTTTTTTTTTTTT	Oy 61 GCACCCCTCCATGCTGCTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 120	181 ACCTTCACTGCCCACACCCCATATGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG	Qy 361 CAAGGTCAGGCAAGAAAAAAAGTAAAGGAAGCAATCTCCCAACTGACCGGGGGACAT 420
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                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Gorilla.

I (bases 1 to 10230)
Mallet,F., Bouton,O., Prudhowme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.

The endogenous retroviral locus ERVWEl is a bona fide gene involve in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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                                               Gorilla gorilla isolate 1 endogenous retrovirus ERV-W, ERVWE1 locus, allele B, complete sequence.
AY101589.1 GI:37544413
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Maller,F., Bouton,O. and Oriol,G.
Submitted (06-MAY-2002) Retrovirology Department, UMR 2142
CNRS-bioMeriaux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69346 cedex 07, France
Location/Qualifiers
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                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality date (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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entire insert of this
    NOTICE: This sequence may not represent the entire insert of this close. I may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between naighboring data submissions.
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                                                                                                                                                                                          MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warre:
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence,
http://genome.wustl.edu
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="7"
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.

The endogenous retroviral locus ERVWEI is a bona fide gene involve in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Pan troglodytes isolate 1 endogenous retrovirus ERV-W, ERVWEI
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Maller,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (06-MAY-2002) Retrovirology Department, UMR 2142
CNRS-bioMeriaux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
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join(248. 810,9255. 9820)
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Best Local Similarity 94.1%;
Matches 1393; Conservative 0
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source

FEATURES

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REFERENCE AUTHORS

PUBMED JOURNAL

TITLE JOURNAL

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 10229)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucottee,G., Durect,L. and Mandrand,B.
The endogenous retroviral locus ERVWEL is a bona fide gene involved
in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                                                                                                                                                                                                           naction, 10229 bp DNA linear PRI 11-FEB-2004 Pan troglodytes isolate 1 endogenous retrovirus ERV-W, ERVWEl locus, allele B, complete sequence.
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AY101587.1 GI:37544409
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Direct Submission.
Submitted (OG-MAY-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
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999 ATAGTCTGCCTACCTCAGGAATATTTTTTTGTCTGTGGTACCTCAGCCTATCGTTGTTTG 8658	AATGGCTCTTCAGAATCTATGTGCTTCCTCTCTTTTAGTGCCCCCTTTTAGTGCCTTTAGTGCTTCTTAGTGCCCCCTTTAGTGCCTTTAGTGCCTTTAGTGCCTCTTAGTGCCTTTAGTGCCTTTAGTGCTTCTTAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	961 CITCCTITIGITATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC 1020 		191 GITACIGACICCCUSCICACCIIGCARGAICANI INCICIACE CONTROL INTO CONTROL	1		139 CTCAGCCATGGATGCCCTGGATTCTCCCCTTCTTAGACCTCTAGAGCTATAATATG 9198 381 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440			AY101588 Gorilla gorilla isolate 1 endogenous retrovirus ERV-W, ERVWE1	locus, allele A, complete sequence. AY101588 AY101588.1 GI:37544411	Gorilla gorilla (gorilla) Gorilla gorilla Bukaryota, Metazoa, Chordata; Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates; Catarrhini, Hominidae, Gorilla.	<pre>1 (bases 1 to 10230) Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G., Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B. The endogenous retroviral locus ERVWEl is a bona fide gene involved</pre>	in hominoid placental physiology Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731–1736 (2004) 14757826 2 (bases 1 to 10230)

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REFERENCE AUTHORS

TITLE

RESULT 16 AY101588 LOCUS DEFINITION

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Amblet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (O6-MAY-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers

JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL

FEATURES

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Hylobates pileatus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
I (bases 1 to 10246)
Manlet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWEl is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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/db xref="taxon:9589"
/cell_type="PBMC"
/note="isolated by PCR; ERVWE1 locus, allele
endogenous_virus: ERV-W"
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (06-MAY-2002) Retrovirology Department,
CNRS-bioMeritaux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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join(248. .254,2843. .9807)

join(248. .254,7579. .9807)

join(248. .254,7579. .9807)

/product="envelope glycoprotein"

/note="putative mRNA transcript 2"

join(248. .254,9242. .9807)

/note="putative mRNA transcript 3; no
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/mol type="genomic DNA"
/isolate="1"
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Pred. No. 0;
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AY101593 10246 bp DNA linear PRI 11-FEB-2004 N Hylobates pileatus isolate 1 endogenous retrovirus ERV-W, ERVWE1 locus, allele B, complete sequence.

RESULT 17
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DEFINITION HYlobatus pileat

us-09-319-156b-9.rge

	AV101592 10248 b Hylobates pileatus isolate 1 e locus, allele A, complete seque AV101592 1 G1:3754419 Hylobates pileatus Hylobates pileatus Eukaryota; Metazoa; Chordata;		Mallet, F., Direct Sub Submitted CNRS-bioMe d'Italie, 1	/mol type="genomic DNA" /isolate="1" /isolation source="PEMC of gibbon 1" /db_xref="faxon:9589" /coll type="PBMC" /note="isolated by PCR; ERVWE1 locus, allele A endogenous_virus: ERV-W"	-tu∕-tu∕-	/note="syncytin" /codom_start==1 /codom_start==1 /product="envel.ope glycoprotein" /protein_id="aAM68171.1" /db_xref=="01:37544420" /db_xref=="01:37544420" /db_xref=="01:3754420" /db_xref=="01:3754420" /db_xref=="01:3754420" /db_xref=="01:3754420" /db_xref=="01:3754420" /db_xref=="01:3754420" /db_xref=="01:3754420" /db_xref=="01:3754420" /db_xref=="01:375420" /db_xref=="0	HIKUNGELVSDIE II TOJAHAVSANUT INCHENITEDINI TOTTITETETETETETETETETETETETETETETETETET
8 6 8 6 8 6 8	RESULT 18 AY101592 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL PUBMED REFERENCE	AUTHORS TITLE JOURNAL FEATURES sourc	LTR	mRNA mRNA mRNA		
181 ACCTTCACTGCCCACACCCATATGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG 240	421 AGCACCCTAGCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACC 480	601 CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA 660	721 AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACGGG 780	841 AATGGCTCTTCAGAATCTATGTGCTTCCTCTCTTAGTGCCCCCTATGACCATCTAC 900  8646 AATGGCTCTTCAGAATCTATGTGCTTCCTCTTAGTGCCCCCTATGACCATCTAC 8705  801 ACTGAACAAGATTATACAATCATGTGCTTCCTCATTCTTAGTGCCCCCTATGACCATCTAC 8705  901 ACTGAACAAGATTATACAATCATGTCGTACCTAAGCCCCACAACAAAAAAGAGTACCATT 960	961 CTTCCTTTGTPATCAGAGCAGCAGTGCTAGGCAGTACTAGGTACTGGCATTGGCAGTATC 1020	GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT	1201 GGAGAAGGTGTTATTATGTTAATCAATCAGAATTGTCAGAAAGTTAAAGAA 1260 

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                                   CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission.
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 alle
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/nol type="genomic DNA"
/isolate="individual 132 allele A"
/db xref="taxon:9606"
/chromosome="7"
/map="701-422"
/sex="female"
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                                                     Score 1338.6;
Pred. No. 0;
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                                                      Query Match
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Matches 1392; Conservative C
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Homo sapiens (human)
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Homo sapiens
Homo sapiens
Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2694)
Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
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Best Local Similarity 93.9%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches
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                                          (2004)
           The endogenous retroviral locus ERVWE1 is a bona fide in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (200°, 14757826
2 (bases 1 to 2694)
Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 4 d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/organism="Homo sapiens"

/mol_type="genomic DNA"

/solate="individual 148 allele B"

/db_xref="taxon:9606"

/chromosome="7"

/map="7421-q22"

/eex="male"

/cell_type="PBMC's"

/note="Caucasian
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/note="splice acceptor site"
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GCACCCCTCCATGCTGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA
           ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC
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1 (Bases I to 269; Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B. The endogenous retroviral locus ERVWEl is a bona fide gene involved in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                            AF520489S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 22 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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Direct Submission
Direct Submission
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/isoTate="individual 22 allele
/db_xref="taxon:9606"
/chromosome="7"
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Fred. No. 0;
0; Mismatches
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/note="Caucasian
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Homo sapiens
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Best Local Similarity 93.9
Matches 1390; Conservative
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KEYWORDS
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YRCLNGSSBSMCFLSFLVPPMTIYTEQDLYNYVISKPRNKRYPILPFYIGAGVIGALG
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FLGPLAAIILLFGPCIFNLLVNFYSSRIEAVKLQMEPRWQSKTKIYRRPUDRPASP
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The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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      GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAAGAA
                                                                      ATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTC
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Direct Submission
Submitted (07-Jun-2002) Retrovirology Department,
CNRS-blomerieux, Ecole Normale Superieure de Lyon
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/organism="Homo sapiens"
/mol type="genomic DNA"
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Location/Qualifiers
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Mallet, F., Bouton, O.
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Homo sapiens (human)
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/note="splice acceptor site"
1959. .2694
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Pred. No. 0;
0; Mismatches
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/note="splice acceptor site"
                                         /map="7q21-q22"
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Direct Submission
Submitted (OrJUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 63934 cedex 07, France
Location/Qualifiers
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'note="syncytin"
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Homo Bapiens individual 55 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.

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AATGGCTCTTCAGAATCTATGTGCTTCCTCTTCTTAGTGCCCCCTATGACCATCTAC
                                                                                                                                                                      GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
                                                  944 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACTCTAACCTGTGTAAATTT
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sapiens (human)

2 of 2 Homo sapiens Homo sapiens

ACCESSION VERSION KEYWORDS SEGMENT SOURCE ORGANISM

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RSDVNDIKGTPPPEELSAAQPLLRNSAGSS"
1705. 1720
                                                                                  Mallet, F. Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Mallet, F., Bouton, O., Duret, L. and Mandrand, B.
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWEl is a bona fide gene involved
in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Maller,Fr., Bouton,O. and Oriol,G.
Maller,Fr., Bouton,O.
Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeritux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
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Pred. No. 0;
0; Mismatches 91;
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/isolate="individual 55 allele B'
/db xref="taxon:9606"
/chromosome="7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mex="female"
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/note="endogenous_virus: HERV-W"
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1959. .2694
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/note="splice acceptor site"
284. .1900
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1 (bases 1 to 2694)
Mallate, P., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                                                                                                                   AF520521S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 6 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
1664 CTACTCCTCTTGGACCCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTCTTCCAGAATC 1723
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- 46 allee
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Direct Submission
Submitted (OrJUN-2002) Retrovirology Department,
CNRS-bioMerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/isolate="individual 6 allele A'/db_xref="taxon:9606"
/chromosome="7"
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 93.9
Matches 1390; Conservative
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBMED
REFERENCE
                                                                                                                                                                                                                                                                      ACCESSION
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AFS20529S2 2694 bp DNA linear PRI 11-FEB-2004 Complete sequence. A complete sequence. AFS20530
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWB1 is a bona fide gene involve in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
1424 CAAAATCGAAGGTTTAGACTTGCTAACCGCTGAAAGAGGGGAACCTGTTTATTA
                                                                                                        GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA
                                                                                                                          CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA
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Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department,
CNRS-bioMeriteux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 63364 cedex 07, France
Location/Qualifiers
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/product="envelope glycoprotein"
/protein_id="AAQ17587.1"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/isolate="individual 78 allele i/db_xref="taxon:9606"
/chromosome="7"
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/note="Caucasian
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2694 bp DNA linear PRI 11-FEB-2004

Homo sapiens individual 71 allele A, envelope glycoprotein gene,
complete cds, and 3' long terminal repeat, complete sequence.

AF520562. GI:33411092
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submitssion
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TVCWTYFTQTGMSDGGGQNDREKHYKEVISQLTRVHGGTSSPYKGLDLSKLHETLRT
HTRLVSLRYTTTGGLHEVSAQNPTNCWICLPLNFRPYVSIPVPEGWNNFSTEINTTSV
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LVGPLVSNLBTTHTGNLTCVKESNTTYYTNSQCIRWVTPPTQIVCLPSGIFFVCGTSA
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Best Local Similarity 93.9%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 91; 1
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Location/Qualifiers
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Homo sapiens syncytin precursor, mRNA, complete cds.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0;
0; Mismatches 91; Indels 0;
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/db_xref="taxon:9606"
930. .2546
/note="unnamed protein product"
                                                                      Keith, J.C., Mccoy, J.M. and Mi, S.
Methods and compositions for diagnosing
and gestational tropholast disorders
abtent: WO 0204678-A 1 17-5AN-2002;
GENETICS INSTITUTE, INC. (US)
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 GI:18620523
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1 (bases 1 to 2930)

Mi,S., Lee,X., Li,X., Veldman,G.M., Finnerty,H., Racie,L.,
LaVallie,E., Tang,X.Y., Edouard,P., Howes,S., Keith,J.C. Jr. and
McCoy,J.M.
Syncytin is a captive retroviral envelope protein involved in human placental morphogenesis

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Direct Submission
Submitted (26-NOV-1999) Genetics Institute, 87 Cambridge Park
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Sha,M., Lee,X., Li,X., Veldman,G.M., Finnerty,H., Racie,L.,
LaVallie,E., Tang,X., Edouard,P., Howes,S., Keith,J.C. Jr.
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3 Jacobs, K., Mccoy, J.M., Lavallie, E.R., Racie, L.A.C., Evans, C., Marberg, D., Mi, S. and Treacy, M.

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PR 18-MAY-1999 JP 2000549638

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PR 18-MAY-1999 US 09/080478, 20-0CT-1998 US 09/175928 PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A COLLINS PI RACIE,

PI CHEXYL EVANS, DAVID MERBERG, SHA MI, MAURICE TREACY PC AGIPS/00, AGIRK45/00, AGIRK45/00, AGIRK45/00, AGIRK45/00, AGIRK45/00, AGIRA5/00, AGIRS/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/00, AGIRA5/0
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C1201/68,C12N15/00,A61K37/02,C12N5/00
C1201/68,C12N15/00,A61K37/02,C12N5/00
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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002515234-A/2.
Homo sapiens (human)
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LOCUS  BD086133  BD086133  BD086133  ACCESSION  BD086133.  BC2613.  BD086133.  BC2613	20-OCT-1998 US 09/175928 PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A COLLINS PI RACIE, PI RACIE, PI CHERYL EVANS, DAVID MERBERG, MAURICE TREACY PC COTK14/47, C12N5/10, C12N15/09, C12P21/02, C12N5/00, C12N15/00 CC Strandedness: Double; CC Topology: Linear; CC Topology	db_xref="taxon:32644"     Ouery Match	Oy 121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATGGAGTTTATCTAAGGGAAACTCC 180  1048 ATGCAGCGTCCCGGAAATATTGATGCCCCGATCTATAGGAGTCTTTTAGGGAACCCCC 1107  Oy 181 ACCTTCACTGCCCACATGCCCCGAACTGCTATAACTTTGCACCCCTTTTGCATG 240  1108 ACCTTCACTGCCCACATATGCCCCGCAACTGCTATAACTTTGCACTGCTCTTTGCATG 1167  Oy 241 CATGCAATACTCATTATTGGACAGGAAAATGATTAATCCTAGTTGCTCCTGGAGGATT 1227  Oy 301 GGAGCCATTATTGGACAGGAAAATGATTAATCCTAGTTGCTCCTGGAGGACTT 1227  Oy 301 GAGCCACTGTTATTGGACTTACTTCACCCAACTGTTGCTCTGGAGGATT 1287  Oy 361 CAAGGCACATGATTACTTCACCCAACTGGTTGTCTGATGGGGGTGGAATT 1287  Oy 361 CAAGGCACATGATTACTTCACCCCAACTGGTTGTCTGATGGGGGTGGAATT 1387  Oy 361 CAAGGTCAGGGAAAAAAAGAAAAGAAAGAAACTACCCCAACTGACCGGGGGAAT 1347  Oy 421 AGCACCCCTAGACCAAAAAGAAAAAAAAAAAAAAAAAAA	Db 1348 GGCACCTCTAGCCCCTACAAAGGACTAGATCTCTCAAAACTACATGAAACCTCCGTACC 1407

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// Mol_type="mRNA"
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25. .x1624
/ codon_start="arxanisma."
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/ translation="malpYHIFLTAHTHWRNCYHSATLCMHANTHYWTGKMINPSCPGGLGV
TVCWTYFTGTGABSDGGGYQDQAREKHWTGYSTCHTGTSSPYKGLDLSKKHHETLRT
HTRLUSLRNTTLTGHLBVSAQNPTNCWTCLPLNFRPYVSIPVPEQWINFSTEINTTSV
IVGPLVSNLETTHTSMLTCVKESNTTYTTNSQLTRWTPPTQTVCLDSGSIFFVCGTSA
YRCLNGSSESMCFLSFLVPPMTIYTEQDLXNYVISKRRNKRYPILPFVIGAVLGALG
TGIGGTTTTSTOPTYCKESONTTYTTNSQLTRWTPPTQTVULONRALDLITAE
RGGTCLFLGEBCCYYNNGSGTYTEKVKEIRDRIQRARELLATGPRASP
RLGGPLAAITLLLLEGPCIFULLVNFVSSRIEAVKLQMEPKMQSKTKIYRRPLDRPASP
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The HERV-W/ng family in the human genome. Potential for protein the HERV-W/ng family in the human genome. Potential for protein capression and gene regulation (2002)

(bases 1 to 1624)

(bases 1 to 1624)

(bases 1 to 1624)

Direct Submission

Submitted (29-APR-2002) U-488, INSERM, 80, rue du General Leclerc, Le Kremlin-Bicetre 94270, France
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                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1624) 111el, P.M., Perin, J.P., Pierig, R., Nussbaum, J.L., Menard, A. and Rieger, F.
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2 (bases 1 to 1624)
Alliel,P.M., Perin,J.P., Goudou,D., Bitoun,M., Robert,B. and
                                                                                                                                          Endogenous retroviruses and multiple sclerosis. II. HERV-7q
C. R. Acad. Sci. III, Sci. Vie 321 (10), 857-863 (1998)
99052087
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Alliel,P.M., Goudou,D., Perin,J.P. and Rieger,F.
Direct Submission
Submitted (10m-WAY-2002) U-488, INSERM, 80, rue du General Leclerc,
Le Kremlin-Bicetre 94270, France
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1860)
Alliel,P.M., Perin,J.P., Pierig,R., Nussbaum,J.L., Menard,A. and
Rieger,F.
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C. R. Acad. Sci. III, Sci. Vie 312, 857-863 (1998)
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/product = fenvelope glycoprotein"
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RSDNNDIKGTPPEELSAAQPLLRPNSAGSS"
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                                    Enkaryofe, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 2694)

Mallat, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.

The endogenous retroviral locus ERVWE1 is a bona fide gene involve in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Direct Submission

Direct Submission

CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2694;
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/organism="Homo sapiens"
/mol type="genomic DNA"
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/sex="female"
/cell type="PBMC's"
/note="endogenous_virus: HERV-W"
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284. .1900
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93.8%; Pred. No. 0;
iive 0; Mismatches
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Db 1604	CTCAGCCAATGGATGCCCTGGATTCTCCCCTTCTAGGACCTCTAGCAGCTATAATATTG 1663	Matches	nes 1389; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
0, 1381	TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440	ò	1 ATGGCCCTCCCTTATCATACTTTTTTTTTTTTTTTTTTT
1664		qq	284 ATGGCCCTCCTTATCATATTTTTCTCTTTACTGTTCTTTTACCCTCTTTTCACTCTCTCA 343
Oy 1441 Db 1724		\$ a	61 GCACCCCCTCCATGCTGCTGTACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 120
RESULT 40 AF520483S2	٠	& 8 	121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC 180
	AF520483S2 2604 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 147 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.	<i>à</i> :	181 ACCTTCACTGCCCACACCCATATGCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG 240
ACCESSION AND VERSION AND KEYWORDS	FS20484.1 GI:33410936	8 &	3 8
ä	2 of 2 Homo sapiens (human)	q	524 CATGCAAATACTCATTATTGGACAGGAAAAATGATTAATCCTAGTTGTCCTGGAGGACTT 583
_	homo Baplens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 2694)	<i>&amp;</i> 8	301 GGAGCCACTGTCGACTTACTTCACCCATACCAGTATGTCTGATGGGGGTGGAATT 360 
AUTHORS ME BC TITLE IN	Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B. He endogenous retroviral locus ERVWE1 is a bona fide gene involved	8 8	361 CAAGGTCAGGCAAGAGAAAAAGAAGGAAGCAATCTCCCAACTGACCCGGGGACAT 420 
JOURNAL P	n nominoid piacental physiciogy roc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004) Arrense	} &	AGCACCCCTAGCCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCCT
SEE	1,5,0,2 (bases 1 to 2694) allet,F., Bouton,O. and Oriol,G.	. a	
TITLE DO JOURNAL SO CI	Direct Submission Submitted (07-JUN-2002) Retrovirology Department, UMR 2142 CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee d'Italie, Lyon 69164 cedex 07. France	ò a	481 CATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCC 540
FEATURES source	Location/Qualifiers 1. 2694 /organism="Homo sapiens"	λŏ	CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTTCAATC 6
	/mol_type="genomic_DNA" /isolate="individual 147 allele B"	අු (	
	/ db_xref="teaxon:9606" /chromosome="17" /map="7q21-q22"	e 6	884 CCTGTACCTGAACAATGGAACAACTTCAGCACAGAATAAACACCACTTCCGTTTTAGTA 943
		ov B	661 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAATTT 720 
CDS	reature // 43. "5/ /note="plice acceptor site" 284. 1900	· &	
	/note="syncytin" /codon_start=1	q Q	1004 AGCAATACTACATACAACCAACCCCAATGCATCAGGTGGGTAACTCCTCCCACAAA 1063
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	HTRIVSLENTILICELHEVSAQNETNCHTCLPLÄRRPYVSI PVPEQWNNFSTEINTTSV LVGPLVSNLEITHTSNLTCVKFSNTTYTTNSQCIRWVTPPTQIVCLPSGIFFVCGTSA	3 음	AATGG
	YRCLNGSBESMČELSFLVPPMTI TIEQDLYS Y U SKYKNKKV PLIJEY V UGAGVJAGLG TGIGGITTSTQFYYKLGQELNGDMRRVADDSLYTLQDQLNSLAVVLQNRRALDLLTAE RGGTCLFLGEECCYYNNQSGI VTEKVKEI RDBI QRRABELRWTGPWGLLSQWMPWI LP FLGPLAAI I LLLLEGPC FRILL VNFVSSR I EAVKLQMEPKMQSKTKI YRR PLDR PASP	λο qα	901 ACTGAACAAGITTATACAATCATGTCGTACCTAAGCCCCACAACAAAAGAGTACCCATT 960 
· misc_feature		۸٥	961 CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCAGTTTGGCAGTATC 1020
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Query Match	1 90.1%; Score 1333.8; DB 9; Length 2694;	ે દે	
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1 GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT 1140	1 CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA 1200	GOGGAAGAATGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA	ATTCGAGATCGAATACAATGTAGAGCGAGGAGCTTCAAAACACCGCAGGGCCTC 1320 	1 CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG 1380	1 TIACTCCTCTTIGGACCCIGIATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440	1 GAAGCTGTAAAGCTACAGATGGACCCCCA 1481 	
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Search completed: February 21, 2005, 11:52:28 Job time : 6367.91 secs Aah20069 HERV-W en Aax25661 Human end Aax59211 5' non co Ade09587 Novel DNA Adf59718 Human con Abn97978 Human ret Abn97931 Human ret

Human gen Human ret Probe #45

foe #46 bre

Acn44334 Human g Abn97930 Human re Aba1608 Probe #4 Aba18590 Probe #4 Aba18592 Probe #4 Aba25978 Probe #4 Aba25978 Human bo Aba20670 Human bo Aba20670 Human bo Aba104629 Probe #4 Aba104629 Probe #4 Aba104639 Human go

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Aax29703 Clone C15
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Aaa63826 Nucleotid
Aaa96625 DNA encod
Adb8400 MSRV-1 as
Aad41225 Human EMB
Aax77526 Human sec
Aaz59468 Human sec
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Abs 1098 Human gen
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Abs 161744 Colon ade
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                                                                                                                                  February 21, 2005, 06:25:25; Search time 763.929 Seconds (without alignments) 11476.370 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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New nucleic acid from retroviruses - useful for diagnosis, prevention and treatment of, e.g. multiple sclerosis.

WPI; 1998-322732/28.

P-PSDB; AAW71068

ADS30988 ABN97929 ABL61744 AAF55630 AAAS9215

10499 56093 2781 7582 7582

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Score

Result

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1461.8

Disclosure; Page 184-185; 286pp; English.

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    The present sequence represents a multiple sclerosis (MS) associated retrovirus (MSRV) genomic fragment used in the method of the invention. The invention provides complete or partial genomic sequences of the MSRV-1 pol gene, gag gene and env gene, and polypeptides encoded by these genes. The invention also provides antibodies raised against the polypeptides. The genomic sequences, polypeptides and antibodies are also claimed useful for diagnosing infection by MS and rheumatoid arthritisassociated viruses, and also for prevention and treatment of infection with these viruses
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(first entry) Clone C15 from MSRV-1. WPI; 1999-098275/09 (INMR ) BIO MERIEUX 

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                                                                             This sequence represents clone C15 from a novel multiple sclerosis related virus type 1 (MSRV1). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis. (Updated on 27-ANG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)
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                          Nucleic acid seguences of retrovirus called MSRV-1 - associated with multiple sclerosis or rheumatoid polyarthritis.
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                                                                                                               The invention relates to an isolated nucleic acid which comprises the gene of a retrovirus associated with multiple sclerosis or rheumatoid arthitis. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthitis. The present sequence is used in the exemplification of the invention.
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                                                      New isolated nucleic acid and their fragments retrovirus, useful for diagnosing, preventing sclerosis and/or rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2; 23pp; English
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Matches 1481; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes an envelope protein of MSRV-1. The envelope protein expressed by the endogenous human retrovirus MRSV-1 has superantigen activity associated with autocimmune disease. The protien can be detected using the method of the invention. The specification describes a process for detecting activity of a superantigen in a biological sample. The process comprises identifying large scale expansion or loss of lymphocytes that carry at least one of the Vbeta16 and/or Vbeta17 determinants. The method is used to screen for agents that inhibit the superantigen, especially those associated with MRSV-1 which is implicated in autoimmune disease, particularly multiple stores.

These agents are potentially useful for treatment or prevention (e.g. as vaccines) of autoimmune diseases
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                                                                                                                                                     Envelope protein; MSRV-1; superantigen; autoimmune disease; Vbetal6;
Vbetal7; multiple sclerosis; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting superantigen activity, useful for identifying agents for treatment or prevention of autoimmune disease, from expansion or loparticular lymphocyte Vbeta determinants.
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Pred. No. 0;
0; Mismatches 12; Indels
an envelope (env) protein of MSRV-1
                                                                                                                                                                                                           Location/Qualifiers
1. .1629
/*tag= a
/product= "envelope protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; Page 123-124; 134pp; French
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Best Local Similarity 99.2%;
Matches 1469; Conservative 0
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                                                                  AAA96625 standard; DNA; 1629
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                                                                                                                                                                                       endogenous retrovirus
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P-PSDB; AAB19069.
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28-OCT-1999;
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primer for the amplification by polymerisation of a nucleic acid of a viral material associated with multiple sclerosis or rheumatoid arbritis, a polypeptide exhibiting an inhibitory activity on the proteolytic, reverse transcriptase or ribonuclease H activity from MSRV, and an antibody directed against the MSRV-1 virus obtained by immunologically reacting a human or animal body or cells with an immunogenic agent consisting of the antigenic polypeptide defined above. The nucleic acids are useful for detecting a biological sample a virus associated with multiple sclerosis or rheumatoid arthritis, or for detecting in a biological sample, the presence of or exposure to a virus associated with multiple sclerosis or rheumatoid arthritis. The present cancinate minimal MSRV-associated sequence whose identity cannot be accurately determined. Note: The SEQ ID numbers for the sequences as a claimed MSRV-associated sequence whose identity cannot be constituted in the main body of the patent do not match the SEQ ID numbers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCACCCTAGCCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCTCCGTACN 480
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                                                                                                                                                                                                                                     sequence listing. Consequently those sequences mentioned in the
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                                                                                                                                                                                                                                                        claims may not be the sequences the authors intended to claim.
                                                                                                                                                                                                                                                                                                                        Length 1481;
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Pred. No. 0;
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Matches 1450; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated or purified nucleic acid associated with multiple sclerosis and/or rheumatoid arthritis, useful for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample.
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JOLIVET-REYNAUD C.
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GARSON J A.
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Komurian-Pradel F,
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/product= "EMBRY-2 protein"
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and mucleic acid molecules encoding such proteins. EMBRY sequences are useful for screening modulators useful for treating or preventing disorders associated with abnormal expression of EMBRY. The disorders treated include reproductive disorders such as infertility, endometriosis, endometrial or ovarian tumour; autoimmune/inflammatory endometriosis, endometrial or ovarian tumour; autoimmune/inflammatory contact dermatitis; disorders of the placenta such as precelampsia, abruptic placentes etc. Sequences of the invention are also useful for analysing a proteome of a tissue or a cell type. EMBRY proteins are useful as immunogens for preparing antibodies. Polynucleotides of the invention are useful disorders. They are also useful is a managenic animals to model human diseases. They are also used in gene therapy. The animals to model human diseases. They are also used in gene therapy. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptides of human embryogenesis associated proteins for screening modulators useful for treating or preventing disorders e.g. endometriosis, infertility, allergy, preeclampsia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to human embryogenesis associated proteins (EMBRY)
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"Mature EMBRY-2 protein'
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Pred. No. 0;
0; Mismatches
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The invention relates to identifying compounds which are modulators of syncytin expression. The syncytin modulators are useful in diagnosis and treatment of precelampsia and gestational trophoblast disorders (e.g. choriocarcinoma, hydatiform mole, placental site tumour and missed, incomplete abortion). Syncytin is a human gene derived from the envelope gene of human endogenous defective retrovirus, HRRV-W. The present invention is based partly on the discovery that syncytin expression is dramatically reduced in precelampsia, and is also mis-localised to the apical syncytiotrophoblast membrane. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a compound for treating a subject with or at risk of developing preeclampsia, comprises determining whether the expression or activity of syncytin in the cell is modulated in the presence of a test
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Pred. No. 0;
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/product= "Syncytin"
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                                                                         AAD24195 standard; cDNA; 2930
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P-PSDB; AAE14540.
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                                               AGCACCCCTAGGCCCTTAGAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACC
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This invention describes novel human secreted proteins encoded by polynucleotides isolated from human adult testes, adult brain, adult blood or adult placenta, or murine adult bone marrow or thymus cDNA libraries. The products of the invention are predicted to have biological activities which would make them suitable for treating, preventing or supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, haemacopoiesis regulating activity, tissue growth activity, among activity, chemotating activity, the superessing activity, activity, chemotating activity, the superessing activity, activity, chemotating chemotatic/chemokinetic activity, activity, receptor/ligand activity, and thrombolytic activity, receptor/ligand activity, and thrombolytic activity, receptor/ligand activity, and tumour invalud suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein; testes; brain; blood; placenta; human; murine; thymus; bone marrow; treatment; prevention; nutrition; cytokine; immune; vaccine; cell proliferation; cell differentiation; suppressor; tumour inhibition; haematopoiesis regulator; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; tumour; cadherin; tumour invasion suppressor; gene therapy; tissue growth; ss.
                                2190 ATTCGAGATCGAATACAACGTAGAGCAGAGGAGCTTCGAAACACTGGACCCTGGGGCCTC
                                                                                                       CTCAGCCCATGGATGCCCTGGATTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATTG
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98US-00080478.
98US-00175928.
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CTTCCTTTTGTTATAGGAGCAGGAGTGCTAGGTGCACAGGTACTGGCGTATC
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                                         GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
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                                                           This is the human secreted protein AJ172 2 nucleotide sequence, obtained from a human adult testes CDNA library. The invention relates to secreted human and murine proteins. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Detection of the levels of the proteins can be used for the diagnosis of e.g. pre-eclampsia, placental pathology or cancer. Agents which modulate the expression or function of the proteins may be used for treating a neoplastic disease and inhibiting metastasis. Other suggested activities include nutritional activity (e.g. in feeds), cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopolesis regulating activity, itsue growth activity, activity, haematopolesis regulating activity,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2946 BP; 858 A; 801 C; 570 G; 717 T; 0 U; 0 Other;
                             Page 107-108; 149pp; English
                             14;
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CATGCAAATACTCATTATTGGACAGGAAAAATGATTAATCCTAGTTGTCCTGGAGGACTT 1227
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protein or BD127 1 6 protein. The polynucleotides are useful for

protein or BD127 1 6 protein. The polynucleotides are useful for

chromosome markers or tags to identify chromosomes or to map related gene

chromosome markers or tags to identify chromosomes or to map related gene

continue. The proteins are useful as amino acid supplement, carbon

source, nitrogen source and carbohydrate source. The proteins are useful

for treating various immune deficiencies and disorders (e.g. severe

combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple

solerosis, systemic lupus erythematosus, rheumatoid atthritis), allergic

reactions (e.g. asthma), myeloid coll deficiencies,

osteoporosis or osteoarthritis, peripheral nervous system diseases (e.g.

peripheral neuropathy, Alzheimer's disease, Parkinson's disease),

coagulation disorders, inflammatory diseases (e.g. systemic inflammatory

response syndrome (SIRS), ischaemiar repertusion injury, Crohn's disease,

coagulation munuity, for inducing bone, cartilage, tendon, ligament and/or

nerve growth or regeneration, for proliferating neural cells and for

regenerating nerve and brain tissue, for inducing fertility and for

combinity ing tumour growth. Proteins are also useful for inducing tendon, and also

mammalian cells (e.g., monocytee, fibroblasts, neutrophils), and also

cuseful as inhibitors of receptor/ligand interactions. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteins A23021 encoded by clone A23021 from human adult colon, and BD12716 encoded by clone BD12716 from human fetal kidney cDNA library, useful for treating e.g. multiple sclerosis and rheumatoid arthritis.
hypersensitivity; regeneration; neural cell proliferation; fertility; tumour; chemokine; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collins-Racie LA, Evans C;
Spaulding V, Carlin-Duckett M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represents cDNA encoding a human secreted protein.
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No. 0;
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Pred. N
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Bowman MR,
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96US-00628364.
96US-00659221.
96US-00664596.
96US-00674231.
96US-0071819.
96US-00721731.
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96US-00721733.
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Treacy M,
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P-PSDB; ADC38777.
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Best Local Similarity
                                                                                                          US2002193567-A1
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cc endogenous retrovirus (HERVs) the full length endogenous provirus which was been located on the long arm of human chromosome 7 (7q21-22) has been designated HERV-W. The present invention describes proteins or peptides (1) having superantigen (SA9) activity comprising the ENV protein (ENV) of HERV-W the surface protein (SU) and transmembrane (TM) sub-units. (I) have neuroprotective activity, and can be used in: vaccines; antisensetherapy; and HERV-W SAG activity-inhibitors. (I) and encoding DNA/RNA are useful for diagnoshing multiple sclerosis (MS) or HERV-W-associated disorders. (I) are also useful for identifying substances (and optionally crecovering) capable of binding to a retroviral superantigen associated with MS, substances capable of binding to a retroviral superantigen of blocking SAG activity and substances capable of blocking SAG activity and substance capable of blocking spable of Generating an immune response devoid of SAG activity and being capable of generating an immune response capable of blocking SAG activity, capable of blocking transcription or capable of blocking transcription or translation of HERV-W retroviral superantigen for use in treating or capable of blocking sAG activity, capable of blocking transcription or translation of HERV-W retroviral superantigen for use in treating or capable of blocking sAG activity, capable of blocking transcription or translation of MS. (I) and nucleic acids encoding them are useful for diagnosing autoimmune disease. The present sequence encodes the specifically claimed envelope protein of HERV-W designated G
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93.8%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human retrovirus HERV-W ENV proteins/peptides having superantigen ivity useful for diagnosing and treating multiple sclerosis.
                                                                                                                                                                                                                                                ATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTC
                                                                                                                                                                                                                                                                     Human endogenous retrovirus; HERV-W; HERV; chromosome 7; env protein; envelope protein; multiple sclerosis-related superantigen; vaccine; surface antigen; transmembrane; multiple sclerosis; neuroprotective; antisense-therapy; autoimmune disorder; ds.
                                                     2068 CAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAGAGGGGGGAACCTGTTTATTTTA
                                                                                                                                                                          GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAAGAA
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/product= "HERV-W envelope protein G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HERV-W envelope protein G coding sequence.
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1. .1617
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P-PSDB; AAB75138.
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disease; HERV-7q; chromosome 7q; immunotherapy;
                                                                              Human retroviral HERV-7q env coding sequence
                    ABN97948 standard; DNA; 2055
                                                                                                                                  Human endogenous retrovirus
                                                           (first entry)
                                                                                                             multiple sclerosis;
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The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q. Regulatory elements associated with HERV-7q may alter expression of ther genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immunotherapy. HERV-7q peptides and their coding sequences can be used in immunogenic or vaccinating compositions, for protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was
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HERV-7q; chromosome 7q; immunotherapy;

Human endogenous retrovirus.

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Autoimmune

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(first entry)

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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE

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Single copy genomic hybridization probes for detecting specific nucleic acid sequences in sample by in situ hybridization useful for detection of

acquired or inherited genetic diseases. Example 1; SEQ ID NO 21; 30pp; English.

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historic call cycle regulation defective, S. cerevisiae homologue A; HIRA; high complexity repeat; in situ hybridisation; Southern blot; chromosome breakpoint; inherited genetic disease; neoplastic disorder; chromosome 22; DiGeorge syndrome; Velo-Cardio-facial syndrome.
                                                                                           high complexity repeat found in the HIRA gene #21
1441 GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA
      2369 GAAGCTGTAAAACTACAAATGGAGCCCAAGATGCAGTCCAA
                                                                                                                                                                                                14-MAY-2001; 2001US-00854867.
                                                                                                                                                                                                               16-MAY-2000; 2000US-00573080.
                                                 ADS30988 standard; DNA; 8523
                                                                              (first entry)
                                                                                                                                                                                                                                                   Knoll JHM, Rogan PK;
                                                                                                                                                                                                                            KNOLL J H M.
ROGAN P K.
                                                                                                                                                                                                                                                                WPI; 2002-062378/08.
                                                                                                                                                                    US2003224356-A1.
                                                                                                                                                      Homo sapiens.
                                                                                              Human genome
                                                                              18-NOV-2004
                                                                                                                                                                                   04-DEC-2003.
                                                                 ADS30988;
                                                                                                                                                                                                                             (KNOL/)
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The invention relates to a nucleic acid hybridisation probe comprising a comparation single copy nucleic acids of at least 50 nucleotides, which will hybridise to a deduced single copy sequence interval in target cucleic acid (TNA) of known sequence. The single copy sequence is deduced copy sequence is deduced copy comparing the target nucleic acid (e.g. a disease causing gene) with a collection of high and low complexity repeat sequences as found in the copy sequence of the organism from containing the target nucleic acid. The probe is generated by PCR on the target sequence. The probe is essentially free cof blocking nucleic acid sequences which will hybridise to repeat copy with a label selected from fluorochrome-responsive labels, fluorochromes, calorimetric chemical, conjugated proteins, antibodies, antigens and their mixtures. The probe is useful in a hybridisation method, where the copy in the in study hybridisation method is from in situ hybridisation, southern blot, and coher methods in which nucleic acid is immobilised, where the method coher method a duplicon or triplicon sequence domain. The probe is useful for for detarmining the avierence of hybridise to a duplicon or triplicon sequence domain. The probe is useful injustings to a unplation. In the property of presence to a unplation of the existence of previously unknown repeat sequence families in a genome. The method comprises reacting a labelled probe with the genome, causing the probe to hybridises and ascertaining if the probe hybridises to the genome at more than three preferably ten different locations as a determination of new repeat sequence family, where the determining step comprises selecting the single copy sequence from a duplicon or triplicon sequence domain. The probe is useful for determining a chromosome breakpoint and is useful in the fields for cytogenetics and molecular genetics for determining the presence of specific nucleic acid sequences in a sample of eukaryotic origin, e.g. the probes may be used to analyse specific chromosomal locations by in situ hybridisation as a detection of acquired or inherited genetic

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                                                                                                                   CTTCCTTTTGTTATCAGAGCAGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC
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       diseases especially for detection of genetic or neoplastic disorders. Unlike prior art techniques, the probe permits more precise chromosomal breakpoint determinations by in situ hybridisation. The genomic sequence comprising the human HIRA gene (histone cell cycle regulation defective, S. cerevisiae, homologue A) was analysed for single copy sequence intervals for use as probes of the invention. HIRA is located on chromosome 22 as a duplicate, deletions of 1 copy lead to Dideorge and velo-Cardio-facial syndromes. The present sequence is a high complexity repeat found within the human genome used to analyse the HIRA gene for repeat found within the human genome used to analyse the HIRA gene for repeat regions. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030224356.
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                                                                                                The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q. Regulatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immunotherapy. HERV-7q peptides and their coding sequences can be used in immunospanic or vaccinating compositions, for protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was used to illustrate the invention
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                               nucleic acid sequences of human endogenous retrovirus, HERV-7q, used diagnosis, treatment and prevention of autoimmune and neurological
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                                                                                Claim 3; Fig 1; 225pp; French
          WPI; 2000-160587/14
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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The present invention describes a method (MI) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result
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of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oseophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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The present sequence encodes a human endogenous retrovirus envelope protein. The specification describes a method for detecting expression of an envelope protein from a human endogenous retrovirus (HENV), in cells, of a tissue or culture. The method comprises detecting syncytia formation due to the fusogenic properties of the envelope protein. Envelope polyphylactic compositions, particularly for treatment of cancer, to correct defects in placental development (or other natural formation of other types of syncytial), and to promote adhesion of cells in grafts or cellular repair processes. Expression of sequences antisense to the polymucleotide are used to prevent formation of syncytial.
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                                                                                Detecting expression of human endogenous retrovirus envelope protein cells of a tissue or culture, from its ability to induce syncytia.
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89.8%; Score 1330.6;

Best Local Similarity 93.7%; Pred. No. 0;

Matches 1387; Conservative 0; Mismatches
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                                                                      CTTCCTTTTGTTATCAGAGCAGGGGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC
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               ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCCACAACAAAAGAGTACCCATT
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syncytia; cancer; cell adhesion; ss.
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'product= "envelope protein"
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(INRM ) INST ŅAT SANTE & RECH MEDICALE
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                                                                                                                                                             The present sequence represents an endogenetic retrovirus, which is associated with an autoimmune disease, and is integrated into the human genome. The retrovirus is human endogenous retrovirus (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. HERV-W nucleic acid fragments, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell proliferation in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
New nucleic acid from human endogenous retrovirus, useful e.g. for diagnosis of autoimmune disease and complications of pregnancy, contains at least part of the gag gene.
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; Pred. No. 0;
24; Mismatches
                                                                                                                     Disclosure; Page 49-52; 53pp; French.
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92.2%;
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Best Local Similarity 92.2
Matches 1365; Conservative
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Autoimmune disease; retrovirus; human endogenous retrovirus W; HERV-W; gag gene; pregnancy; multiple sclerosis; T cell proliferation; ss.

Location/Qualifiers

Human endogenous retrovirus

Human endogenous retrovirus W (HERV-W) sequence.

(first entry)

07-NOV-2000

ВР

DNA; 7582

standard;

AAA59215

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This sequence represents the complete sequence of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulin- dependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
                                                                                                                                                                                                                                                                                                                                                       Clone; human endogenous retrovirus; genome; autoimmune disease; multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diabetes; disseminated lupus erythematosus; pregnancy; chromosomal marker; ss.
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ATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGGAACGCTGGGGCCTC
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(pos:790. 792, aa:Phe)

(pos:1912. 314, aa:Thr)

(pos:812. 864, aa:Thr)

(pos:818. 820, aa:Ser)

(pos:865. 864, aa:Thr)

(pos:107. 1176, aa:Arg)

(pos:1903. 1905, aa:Ibu)

(pos:2017. 2019, aa:Ibu)

(pos:2017. 2019, aa:Ibu)

(pos:2017. 2019, aa:Ibu)

(pos:2026. 2012, aa:Arg)

(pos:2086. aa:Arg)

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(pos:2089. 2011, aa:Ibu)
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New human retrovirus HERV-W ENV proteins/peptides having superantigen activity useful for diagnosing and treating multiple sclerosis.

Claim 13; Fig 9; 94pp; English

Con the basis of the PBS t-RNA motif used for the classification of human endogenous retrovirus (HERVS) the full length endogenous provirus which endogenous retrovirus (HERVS) the full length endogenous provirus which endogenous retrovirus (HERVS) the full length endogenous proteins which designated HERVYW. The present invention describes proteins or peptides of HERVYW, the surface protein (SU) and transmembrane (TM) sub-units. (I) having superantigen activity, and cransmembrane (TM) sub-units. (I) have neuroprotective activity, and can be used in: vaccines; antisensetherapy; and HERVYW SAG activity-inhibitors. (I) and encoding DNA/RNA are useful for diagnoshing multiple sclerosis (MS) or HERVYW and optionally recovering) capable of binding to a retroviral superantigen associated with MS; substances capable of blocking SAG activity and substances capable of blocking transcription or translation of HERVW retroviral superantigen associated derived from (I), modified to be devoid of SAG activity and being capable of generating an immune response against HERV-W retroviral superantigen associated with MS; or capable of blocking SAG activity, capable of blocking transcription or translation of HERV-W retroviral superantigen associated with MS; or capable of blocking transcription or translation of HERV-W retroviral superantigen sasciated with MS; or capable of blocking transcription or translation of HERV-W retroviral superantigen for use in treatment and preventing MS. (b) and nucleic acide encoding them are useful for diagnosing autoimmune disease. The present sequence encodes the georifically claimed envelope protein of HERV-W designated G encoding them are useful for specifically claimed envelope protein of HERV-W designated G

Sequence 2782 BP; 741 A; 768 C; 564 G; 709 T; 0 U; 0 Other;

1002 1062 1122 ö 240 300 360 420 120 180 942 822 882 9 ATGGCCCTCCCTTATCATATTTTCTCTGTAGTGTTCTTTCACCCTGTTTCACTCTCACT 823 GCACCCCCCCCATGCCGCTGTATGACCAGTAGCTCCCCTCACCCAGAGTTTCTATGGAGA Arecaecerceegaaararreareceeareeraraeaacrerrreraageaaceee ACCTTCACTGCCCACACCCCATATGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG Accricacideceacacacataraceceacaaciderareacidecacacitrificare GGAGTCACTGTTGGTTGGACTTACTTCACCCAAACTGGTATGTCTGATGGGGGGTGGAGTT AGCACCCCTAGGCCCTACAAAGGACTAGTTCTCTCAAAAACTACATGAAACCCTCCGTACC GCACCCCTCCATGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC CATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTAGTTGTCCTGGAGGACTT GGAGCCACTGTCTGTTGGACTTACTTCACCCATACCAGTATGTCTGATGGGGGGTGGAATT CAAGGTCAGGCAAGAAAAAAAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACAT ATGGCCCTCCCTTATCATACTTTTCTCTTTACTGTTCTCTTACCCCCTTTCGCTCTCACT Gaps DB 5; Length 2782; .; 0 Indels 108; Query Match 88.3%; Score 1308.2; Best Local Similarity 92.7%; Pred. No. 0; Matches 1373; Conservative 0; Mismatches 943 1003 1063 1123 Н 121 61 883 181 361 421 241 301 Query Match 셤 셤 ò g g ઠે 요 g ò ò ઠે 원 8 ò ò

1380 1440 1260 1320 2143 CTACTCCTCTTTGGACCCCTGTATCTTTGACCCTTGTTAACTTTGTCTCTTCCAGAATC 2202 1140 1902 1200 1962 2022 2082 1020 1782 1080 1842 CCTGTACCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCCACTTCCGTTTTAGTA 1422 1482 1542 1602 1662 1722 840 900 960 600 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT.720 crcasccsarsestreccresarrerecerrerrassacereraseseraraarare 1381 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATT 1423 GGACCTCTTGTTTCCAATGTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT 1483 AGCAATACTACATACACAACCAACCCAATGCATCAGGTGGGTAACTCCTCCCCACACA AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTAGTGCCCCCTATGACCATCTAC ACTGAACAAGATTTATACAGTTATAGTCATATCTAAGCCCCGCAACAAAAGAGTACCATT crirciriridriana galacca de de contra de contr ACAACCTCTACTCAGTTCTACTACAAACTATCTCAAGAACTAAAATGGGGACATGGAACGG GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA ATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTC 2023 ATTCCAGATCGAATACAACGTATAGCAGAGGAGCTTCGAAACACTGGAGCCCTGGGGCCTC CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTTAGGACCTCTAGCAGCTCTAATATTG 1243 CATACTCGCCTGGTAAGCCTATTTAATACCACCTCACTGGGCTCCATGAGGTCTCGGCC 1303 CAAAACCCTACTAACTGTTGGATATGCCTCCCCCTGAACTTCAGGCCATATGTTTCAATC AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCCTCCCACGA ATAGTCTGCCTACCCTCAGGAATATTTTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTG ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCCACAACAAAAGAGTACCCATT CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTTGGCAGTATC CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCCACTTCCGTTTTAGTA 2243 1441 GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481 1021 1843 1141 1903 1363 1543 1603 1663 1723 1783 1081 1963 1261 1321 2083 2203 721 781 841 901 961 1201 481 541 601 661 g g 원 ò g ઠે g ò g à 셤 à g g ò g ò ò g ò ò 셤 g ò g ð 셤 ò ò ò

RESULT 22 AAX25661 ΩI

AAX25661 standard; cDNA to mRNA; 2782

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                                                                                                     Clone; human endogenous retrovirus; genome; autoimmune disease; multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diabetes; disseminated lupus erythematosus; pregnancy; chromosomal marker; ss.
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Pred. No. 0;
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                                                                              endogenous retrovirus W clone cl.PH74
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Best Local Similarity
Matches 1372; Conserv
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                                                CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTCAATC
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                                                                                                                                        gene, and 3' non coding sequences of HERV-W.
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                             CTCAGCCGATGGATGCCCTGGATTCTCCCCTTTAGGACCTCTAGCAGCTATAATATTG 2142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynuclectides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                        Wang J;
Wang Z;
                   TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT
                                                                                                                                                                                                       novel gene; novel protein; tissue marker; molecular weight marker;
chromosome marker; genetic disorder; contig; ds.
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ou P, Drmanac RT,
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                                                          GAAGCIGIAAAGCIACAGAIGGICITACAAAIGGAACCCCA 1481
                                                                     2203 GAAGCTGTGAAAACTACAAATGGAGCCCAAGATGCAGTCCAA 2243
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Weng G, Zhou P,
Boyle BJ;
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Ghosh M, Xue AJ, Wehrman T, Wei
Ma Y, Wang D, Chen R, Xu C, B
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; 2001US-0339453P.
; 2002US-0365991P.
; 2002US-0365384P.
; 2002US-037281P.
; 2002US-0012658.
                                                                                                                             standard; DNA; 3464
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24-APR-2002;
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                                                             ACGCGGCTTCCTGGAAATATTGATGCCCCATCATAAGGAGTTTATCTAAGGGAAACTCC
GCACCCCTCCATGCTGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA
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(I). The polynucleotides (I) can be used as hybridisation probes, oligomers or primers, for chromosome or gene mapping, for the recombinant production of proteins, and for generating antisense DNA or RNA. The present sequence represents a human contig polynucleotide sequence, which is used in an example from the present invention.
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                         GTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAACGCTGAAAGAGGGGGAACCTGTTTA
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                                                                                                                                                              AAAGAAATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACGCGAACGCTGG
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                                                                                                                                                                                                                                                                                                                    Sequence 46340 BP; 16104 A; 8738 C; 8434 G; 13064 T; 0 U; 0 Other;
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15; Page 186-199; 225pp; French
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Best Local Similarity 92.3%;
Matches 1395; Conservative (
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The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q. Regulatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immunotensponse, e.g. in immunotherapy. HERV-7q peptides and their coding sequences can be used in immunogenic or vaccinating compositions, for protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, endogenous retroviruses that are abnormally expressed in cancer, used to illustrate the invention
                                                                                                                                 New nucleic acid sequences of human endogenous retrovirus, HERV-7q, us-
for diagnosis, treatment and prevention of autoimmune and neurological
                                                   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                            Claim 3; Page 134; 225pp; French.
                                                                                                          WPI; 2000-160587/14.
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                                                    Gaps
                                                  32;
                           Length 1799;
Sequence 1799 BP; 488 A; 331 C; 482 G; 498 T; 0 U; 0 Other;
                                                    87; Indels
                           DB 3;
                          Score 1278.8;
Pred. No. 0;
0; Mismatches
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                            Query Match
Best Local Similarity 92.1%;
Matches 1393; Conservative
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chromosome 7q; immunotherapy;

disease; HERV-7q;

retroviral

Human

multiple sclerosis;

Autoimmune

(first entry)

01-AUG-2002

ABN97931

Human endogenous retrovirus

29-DEC-1999

BP.

ABN97931 standard; DNA; 1799

Cytostatic; carcinoma; lymphoma; cancer; human; gene;

WO2003073826-A2. Homo sapiens

12-SEP-2003

genomic sequence hCG32959

Human

(first entry)

18-NOV-2004

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of bioactive agent capable of bioactive agent capable of modulating the activity of CAP; (iii) for screening of a bioactive agent capable of amodulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vii) for inhibiting the activity of CAP; (vii) for treating carcinoma; (vii) for neutralizing the activity of CAP; (vii) for treating carcinoma (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number in addition, the CA genes are useful as DAA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to novel DNA and protein sequences which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 161334 BP; 46474 A; 28689 C; 31549 G; 54602 T; 0 U; 20 Other;
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide sequence.
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92.5%;
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The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q.

Regulatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immune response, e.g. in immunotherapy. HERV-7q peptides and their coding sequences can be used in immunogenic or vaccinating compositions, for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid sequences of human endogenous retrovirus, HERV-7q, use for diagnosis, treatment and prevention of autoimmune and neurological
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                                                                                                                                                                                                                                                   HERV-7q; chromosome 7q; immunotherapy;
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                    gene expression analysis in human cervical cell sample.
                                                                                            CTAGGAGCTCTAATATTGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAG
                   ACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAAC
                                                                                                                                      microarray; gene expression; cervical epithelial cell;
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                                                    ACCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGT
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Pred. No. 0;
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-02346BTP.
27-SEP-2000; 2000US-02346BTP.
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                                                                                                          CCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGTTCTCCCCCTTCTTAGGACCTC
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Db   1065 CCGAGAAAGTTAAAGAAATTCAAGGTCGAATATAACGTAGAGCAAAAGGAGCTGCAAAACA   1304 CCGAACGCTCGGGCTCCTCTGGCGATGCCTCCCTTTTAGGACCTC	RESULT 32 AA135980 ID AA135980 standard, DNA, 1894 BP. xx	AC AAI35980; XX XX DT 17-OCT-2001 (first entry)		Homo sapiens.		04-FEB-2000; 26-MAY-2000;	FR 35-000 200003-000003-000003-00003-00003-00003-00003-00003-00003-000003-00003-00003-00003-00003-00003-00003-00003-00003-00003-00003-00003-00003-00003-0000	(MOLE-) MOLECULAR DYNAMICS INC.	Penn SG, Hanzel DK, Cnen W, Kank DK; WPI; 2001-488897/53.	Human genom gene expres Claim 25; S	C The present invention relates to single exon nucleic acid probes (SE) CC The present sequence is one such probe. The probes are useful for CC producting a microarray for predicting, measuring and displaying gene	for antenat. Sequence 18	Query Match 76.4%; Score 1131.6; DB 4; Length 1894; Best Local Similarity 92.4%; Pred. No. 0; Matches 1218; Conservative 0; Mismatches 84; Indels 16;	Qy 164 TATCTAAGGGAAACTCCACCTTCACCGCCACACCCATATGCCCCGCAACTGCTATAACT	Oy 224 CTGCCACTCTTTGCATGCATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTA
	404 AACTGACCGGGGGACATAGCACCCCTAGCACAAGGACTAGTTCTCTCAAAACTAC 463 	464 AIGAAACCTCGTACCCATACTCGCTGGTGAGCCTATTTAATACCACCTCACTCGGC 523 	524 TCCAIGAGGICTCAGCCCAAAACCCTACTAACIGTIGGATGTGCCTCCCCCTGCACTTCA 583 	OY 584 GGCCATACATTCAATCCTGTTCTGAACAATGGAACAACTTCAGCACAGAAATAAACA 643	OY 644 CCACTICCGITITAGIAGGACCICTIGITICCAAICIGGAAATAACCCAIACCTCAAACC 703 Db 468 CCACTICIGITITAGIAGICCICITICCAAICIGGAAATAACCCAIACCICAAACE 524	Qy       704 TCACCTGTGTAAAATITAGGAATACTATAGACACACAACCAGGCTCCCAATGCATCAGGTGGG       763         Db       525 TCACCTGTGTAAAATITAGCAATACTATAGACACAACACCCCAATGCATGCTAGGTGGG       584	OY 764 TAACACCTCCCACACGAATAGTCTGCCTACCCTCAGGAATATTTTTTGTCTGTGGTACCT 823 Db 585 TAACTCCTCCCACACGAATAGTCTGCCTACCCTCAGGAATATTTTTTTT	Qy 824 CAGCCTATCATTGATTGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGC 883	Qy         884         CCCCTATGACCATCTACACTGAAGATTTATACAATCATGTGGTGCTACCTAAGGCCCACA         943           Db         705         CCCCTAAGCCCATCTACACTGAACAACAATTTATACAATCATGTCATACCTAAGCCCGGCA         764	944	OY 1004 CTGGCATTGGCAGTATCACAACCTCTACTCAGTTCTACTACAAACTATCTCAGAAATAA 1063 	Qy 1064 ATGGTGACATGGAACAGGTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCC 1123 Db 885 ATGGTGACATGGAATGGGTCGCTGATACCCTGGTCACCTTGCAAGATCAACTCCC 944	Qy 1124 TAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGGGGG 1183	Qy 1184 GAACCTGTTTATTTTAGGAGAACGCTGTTATTATGTTAATCAATC	1244 CTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACA 1303

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76.4%; Score 1131.6;
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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27-SEP-2000; 2000US-0236359P.
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived nucleic acid probes for measuring gene expression in a sample derived concletion than breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this partent did not form part of the prince apecification, but was obtained in electronic format directly from WIPO at the princes.
                                       New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
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IGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGT
                                                                                                                                                                                                                                       Human; microarray; single exon probe; gene expression; breast;
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                                                                                                                                                                                                        CTGGACCCTGGGGCCTCCTCACCAATGGATGCCCTGGATTCTCCCCTTCTTAGGACCTC 1184
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03-MG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0235359P.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000;
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Query Match
76.4%; Score 1131.6;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 1218; Conservative 0; Mismatches
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30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234587P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
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                          16;
           Length 1894
                                        TATCTAAGGGAAACTCCACCTTCACTGCCCACACCCATATGCCCCGCAA
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           Score 1131.6;
Pred. No. 0;
                         Mismatches
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            76.4%;
                          Conservative
           Query Match
Best Local Similarity
Matches 1218; Conserv
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                                                                                                                                                                                                                                                  probes useful for analyzing
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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Best Local Similarity 92.4%;
Matches 1218; Conservative
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           1 TATCTAAGGGAACCCCCACCTTCACTGCCCACACACTATGCCCCACAACTGCTATAACT
                                      CTGCCACTCTTTGCATGCATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTA
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                                                                                                                                      Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
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Pred. No. 0;
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Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;	<u> </u>	1244 CTGAGAAAGTTAAAGAAATTCGAGATACAATGTAGAGCAGAGGAGCTTCAAAACA 1303	3 8
		1184 GAACCTGTTTATTTTTAGGAGAAGAACGCTGTTATTATGTTAATCAATC	<u>ڄ</u> ۾
		TAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAGACT	<b>3</b> 8
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specialization (or complements), inspirate the processive special stringency to a nucleic acid molecule expressed in the human stringency to a nucleic acid molecule expressed in the human (I) may be used for predicting, measuring and displaying gene (I) may be used for predicting, and advantaged to the processive of the control of the		1064 ATGGTGACATGGAACAGGTCACTGACTCACCTTGCAAGATCAACTTAACTCCC 1123	<b>∂</b> €
		CTGGCATTGGCGGTATCACAACCTCTACTCAGTTCTACTACAAACTGTCTCAAAAACTAA	qq
	<u></u>	CTGGCATTGGCAGTATCACAACCTCTACTCAGTTCTACT	8
Claim 1; SEQ ID NO 4660; 658pp; English.	XX PS	sakaractakacca	qo
Human genome-derived single exon nucleic acid probes useful gene expression in human adult liver.	I I		ò
WPI; 2001-488898/53.		705 CCCCTATGCCCATCTACACTGAACAAGATTTATACAATCATGTCATACCTAAGCCCCGCA 764	qq
Penn SG, Hanzel DK, Chen W, Rank DR;		884 CCCTATGACCATCTACACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCACA 943	ò
(MOLE-) MOLECULAR DYNAMICS INC.	- AA		3 8
04-0CT-2000;		824 CAGCCTATCATTGTTTGAATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGC 883	ò
30-JUN-2000; 2000US-U0608408. 03-AUG-2000; 2000US-00632366. 21-SEP-2000; 2000US-0234687P.		764 TAACACCTCCCACACGAATAGTCTGCCTACCCTCAGGAATATTTTTGTCTGTGGTACCT 823 [	දු පු
04-FEB-2000; 26-MAY-2000;	AX R	525 TCACCIGIGIAAAATTTAGCAATACTATAGACACAGCCAACTCCCAATGCATCAGGTGGG 584	: ପ୍ର
30-JAN-2001; 2001WO-US000664.			ò
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Human; single exon nucleic acid probe; liver; cirrhosis; hyperlipoprocetinaemia; hyperlipidaemia; hypercholesterolaemia coronary heart disease; 88.	M. M. M.	TCCATGAGGTCTCGGCCCAAAACCCTACTAACTGTTGGA	qa
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1065 CCGAGAAAGTTAAAGAAATTCAAGGTCGAATATAAACGTAGAGCAAAGGAGCTC	<b>q</b> a		

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ugle exon nucleic acid probe (SENP) (I) for on in a sample derived from human adult by defined nuclectide sequences given in the life fragments). The probe hybridises at high molecule expressed in the human adult liver. It adult liver the genes identified may be leases such as cirrhosis, ipidaemia and hypercholesterolaemia which is the desase. ABS2501-ABS25105 represent human d probes of the invention. Note: The patent does not appear in the printed in electronic format directly from WIPO at
                                          CAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTC 1363
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GGTCGAATATAACGTAGAGCAAAGGAGCTGCAAAACA 1124
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    Length 1894;
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  Score 1131.6;
Pred. No. 0;
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ilarity 92.4%;
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                      Best Local Similarity
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1363 1423 CIGGACCTIGGGGCCTCCTCAGCCAATGGATGCCCTGGATTCTCCCCCTTCTTAGGACCTC 1184 The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, breast. The probes are useful for predicting, diagnosing, grading, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and noncarcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences expression in Probe, human, breast disease, breast cancer, development disorder, ss, inflammatory disease, proliferative breast disease, non-carcinoma tumour. TIGICITITICCAGAATCGAAGCAGTAAAACTACAAATCGTTCTTCAAATGGAGCCCCA 1302 TIGICITICCAGAATIGAAGCIGIAAAGCIACAGAIGGICTIACAAAIGGAACCCCA 1481 cccacaaaacrraaacaarrcaaccrccaararaaccracaaccaaaccacaaaca CTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACA TAGCAGCTCTAATATTGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGT CCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTC used to measure gene expression in human breast sample. gene measuring

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TIGICICITICCAGAATIGAAGCIGIAAAGCIACAGAIGGICTIACAAAIGGAACCCCA 1481
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                                                                                                                          TAGCAGCTCTAATATTGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGT
                                                                                                                                                                                                                                                                                                                     Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicoytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary dyskinesis; pulmonary hypertension; hypaline membrane disease.
                                                          CTGGACCCTGGGGCCTCCTCAGCCAATGGATGCCCTGGATTCTCCCCTTCTTAGGACCTC
                                                                                                                                      CTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACA
                                                                                   CCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGTTCTCCCCCTTCTTAGGACCTC
     exon probe from lung SEQ ID No 4580
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26-MX-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0033346.
21-SEP-2000; 2000US-023468TP.
27-SEP-2000; 2000US-023468TP.
04-OCT-2000; 2000GB-0024283.
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probes,

CC complements or the 12387 open reading frames derived from the 12614

Cybobes. Also included are a microarray comprising the novel set of probes

c i the novel set of probes which hybridise at high stringency to a nucleic

acid expressed in the human lung; measuring gene expression in a sample

CC acid expressed in the human lung; measuring gene expression in a sample

CC collection of detectably labeled nucleic acids derived from human lung

CC algorithmically predicting at least one exon from genomic sequences of

the eukaryote; and (b) detecting specific hybridisation of detectably

CL labeled nucleic acids from eukaryote; genome, comprising (a)

algorithmically predicting at least one exon from genomic sequences of

the eukaryote; and (b) detecting specific hybridisation of detectably

CL shabeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

CM having a fragment identical to the predicted exon, the probe is included

in the above mentioned microarray; assigning exons to a single gene,

C comprising (a) identifying exons from genomic sequence by the method

above and (b) measuring the expression of each of the exons in several

CC tissues and/or cell types using hybridisation to a single exon

comprising a probe with the exon, where a common pattern of

microarrays having a probe with the exon, where a common pattern of

concorsishon of the exons in the tissues and/or cell types indicates that

CC fills sequences, mentioned in the specification, or encoded by the

concor, chronic obstructive pulmonary disease (COPD), interstitial lung

cancer, chronic obstructive pulmonary disease (COPD), interstitial lung

disease (LID), familial ideopathic pulmonary disease such as asthma, lung

cancer, chronic obstructive pulmonary disease (COPD), interstitial lung

cancer, chronic obstructive pulmonary disease.

CC probes/open reading frames (ORF)

concorsis, lymphangioleionyomens and hyaline membrane disease. The

CR fargeners syndrome, fibrocyetic pulmonary dysplasia, primonary

cyntensed syndrome ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;

467 583 283 343 167 403 227 463 523 407 643 228 AACTGACCTGGGTACATAGCACCCCTGGCCCCTACAAAGGACTAGATCTCTCAAAACTAC 287 9 CTGCCACTCTTTGCATGCATGCAAATACTCATTATTGGACAGGAAAAACGATTAATCCCA 288 ATGAAACCCTCCATACCCATACTGGCCTGGTAAGCCTATTTAATACCACCCTGACTGGGC TCCATGAGGTCTCAGCCCAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCA TCCATGAGGTCTCGGCCCAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTTA GGCCATACATTTCAATCCCTATACCTGAACAATGGAACAACTTCAGCACAGAAATAAACA 164 TATCTAAGGGAAACTCCACCTTCACTGCCCACACCCCATATGCCCCGCAACTGCTATAACT TATCTAAGGGAACCCCCCACCTTCACTGCCCACACCCCATATGCCCCACAACTGCTATAACT CTGCCACTCTTTGCATGCATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTA CTGATGGGGGTGGAATTCAAGGTCAGGCAAGAGAAAAACAAGTAAAGGAAGCAATCTCCC CTGATGGGGGTGGAGTTCAAGATCAGGCAACAGAAAAACACATAAAGGAAGTAATCTCCC **AACTGACCCGGGGACATAGCACCCCTAGCCCCTACAAAGGACTAGTTCTCTCAAAACTAC** ATGAAACCCTCCGTACCCATACTCGCCTGGTGAGCCTATTTAATACCACCTCACTCGGC GGCCATACATTTCAATCCCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACA Gaps Ouery Match 76.4%; Score 1131.6; DB 6; Length 1894; Best Local Similarity 92.4%; Pred. No. 0; Matches 1218; Conservative 0; Mismatches 84; Indels 16; 224 168 121 344 524 61 284 404 464 584 임 a 움 8 셤 ઠે 셤 δ ઠે ઠે 셤 ઠે g δ

1183 1243 1423 1003 1123 945 TAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAACCGCGGAAAGCGGGG 1004 CCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGTTCTCCCCCTTCTTAGGACCTC 1363 creeacccreeeeccrccrcaeccaaresareccreearrercreecrrerradaaccre TAGCAGCTATAATATTGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGT 1244 524 763 584 823 644 883 704 943 764 824 944 Clone, human endogenous retrovirus, genome, autoimmune disease, multiple sclerosis, rheumatoid polyarthritis, insulin-dependent diabetes; disseminated lupus erythematosus, pregnancy; chromosomal marker; ss. TIGICITICCAGAATIGAAGCIGIAAAGCIACAGAIGGICITACAAAIGGAACCCCA 1481 TIGICTITICCAGAATCGAAGCAGTAAAACTACAAATCGTTCTTCAAATGGAGCCCCA 1302 TCACCTGTGTAAAATTTAGCAATACTATAGACACACCCAACTCCCCAATGCATCAGGTGGG CCCCTATGCCCATCTACACTGAACAAGATTTATACAATCATGTCATACCTAAGCCCCGCA ACAAAAGAGTACCCATTCTTCCTTTTGTTATCAGAGCAGAGTGCTAGGCAGACTAGGTA 765 ACAAAGAGTACCCATTCTTCCTTTTGTTAGAGCAGGAGTGCTAGGCGGAGTAGCTA CTGGCATTGGCGGTATCACAACCTCTACTCAGTTCTACTACAAACTGTCTCAAGAACTAA TAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGG 1005 GAACCTITITATITITIAGAGGAAAAATGCTGTIGTTATGTTAATCAATCCGGAATCATCA CTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGGAGGAGGTTCAAAACA TAGCAGCTCTAATATTGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGT TCACCTGTGTAAAATTTAGCAATACTATAGACACACCAGCTCCCAATGCATCAGGTGGG TAACACCTCCCACACGAATAGTCTGCCTACCCTCAGGAATATTTTTTGTCTGTGGTACCT CAGCCTATCATTGTTTGAATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGC CCCCTATGACCATCTACACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCACA CTGGCATTGGCAGTATCACAACCTCTACTCAGTTCTACTACAAAACTATAAAGAAATAA ATGGTGACATGGAACAGGTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCC Aregreacaresaarescreecrearaccerescreecriscaasareaacreece Human endogenous retrovirus W clone cl.24.4. BP AAX25659 standard; cDNA to mRNA; 1948 Human endogenous retrovirus (first entry) 944 1004 1064 885 1065 1304 1185 468 585 705 1124 1184 1244 1125 1364 1424 1245 525 645 884 825 704 764 824 AAX25659 RESULT 40 임 ò 셤 셤 ò g ò 셤 ò qq ò 쉽 ò a à g ò g ò g ò a à g ò a ò

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1259 CAAAACCCTACTAACTGTTGGATATGCCTCCCCCTGAACTTCAGGCCATATGTTTCAATC
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                                                                                                                                                                                                                                                                                                                                                       This sequence represents clone cl.24.4 of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulindependent diabetes and related pathologies) and of abnormal or susceptibility to these conditions, or proximity markers for associated with this susceptibility
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                                                                                                                                                                                                                                                      New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
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Sequence 17382, A
Sequence 15858, A
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Sequence 2, Appli
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Sequence 12249, A
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Compugen Ltd.
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## ALIGNMENTS

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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHY
THERAPEUTIC PURPOSES
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ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: US/08/979, 847B
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979, 847B
FILING DATE: 26-No. 6582703-1997
CLASSIFTATION NUMBER: 30.024
REFEISTRINGS WILLIAM P.
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KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BENNARD
GARSON, JEREMY
TUKE, PHILIP
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MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-08-979-847B-105
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STREET: P.O. BOX 19928
CITY: ALEXANDRIA
Sequence 105, Application US/08979847B Patent No. 6582703 GENERAL INFORMATION:
                                                                                                                                                         APPLICANT: PERRON, HERVE
BESEME, FREDERIC
BEDIN, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS
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1021		1201 GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA 1201 ATTCGAGAATCGATACAATGCAGAGGGGTTCAAAACACCGAACGCTGCGGCCTC	Db 1261 ATTCGAGATCGAATACAATGTACACAGAGAGCTTCAAAAACACCGAACGCTGGGGCCTC 1320  Qy 1321 CTCAGCCAATGGATGCCCTGGGTTCCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG 1380  Db 1321 CTCAGCCAATGGATGCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG 1380	OY 1381 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440  Db 1381 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440  1441 GAAGGTGTTAACAGATGGTCTTACAAATGGAACCCCA 1481	1441 GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA	RESULT 2 US-09-175-928-3 ; Sequence 3, Application US/09175928A : Parent No. 6112921	GENERAL INFORMATION: APPLICANT: Jacobs, Kenneth SPPLICANT: MCCOY, John M. APPLICANT: LaVallie, Edward R.	Collins-Racie, Li Evans, Cheryl Merberg, David Treacy, Maurice	APPLICANT: Mi, Sha ; APPLICANT: Genetics Institute, Inc. ; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM ; FILE REFERENCE: 6006B.AJJ72A	CURRENT APPLICATION NUMBER: US/09/175,928A; CURRENT FILING DATE: 1998-10-20; NUMBER OF SEQ ID NOS: 62; SOFTWARE: Patentin Ver. 2.0		US-09-175-928-3 Query Match 90.2%; Score 1335.4; DB 3; Length 2946;	vative 0; Mismatches 91; Indels 0; Gaps corrateAractrification of CarrateAractrification of Carr		DD 988 GCACCCTCCATGCCGCTGTATGACCAGTAGCTCCCTTACCAAGAGTTTCTATGGAGA 1047  Qy 121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATAGGAGTTTATCTAAGGGAAACTCC 180
Query Match         100.0%;         Score 1481;         DB 4;         Length 1481;           Best Local Similarity 100.0%;         Pred. No. 0;         0;         Indels 0;         Gaps 0;           Matches 1481;         Conservative 0;         Mismatches 0;         Indels 0;         Gaps 0;           Qy         1 ATGGCCCTCCCTTATCATACTTTTTCTTTTACTGTTCTTACCCCTTTCGCTCACT 60         Db 1 ATGGCCCTCCCTTATCATATTTTCTCTTTACTGTTCTTTACCCCCTTTCGCTCACT 60	61 GCACCCCCTCCATGCTGCTGTACCACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 	121 ACGCGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC	Oy         181 ACCTTCACTGCCCACACCCATATGCCCCGCAACTGCTCACTCTTTCATGCATG	Db 241 CATGCAAATACTCATTATTGGACAGGGAAAATGATTAATCCTGGTGTTGTCTGGGGGTT 300 Qy 301 GGAGCCACTGTCTGTTGGACTTACTTCACCCATACCAGTAGTGTGTGGGGGTGGAATT 360	Oy 361 CAAGGTCAGGAAGAAAAACAAGTAAAGGAATCTCCCAACTGACCGGGGACAT 420 	Qy 421 AGCACCCCTAGCCCCTACAAAGACTTCTCTCAAAACTACATGAAACCTCCGTACC 480 	OY 481 CATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCC 540	OY 541 CAAAACCCTACTAACTGTTGGATGTCCCCCCTGCACTTCAGGCCATACATTCAATC 600	OY 601 CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA 660 1	OY 661 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACACCTGTGTAAAATT7 720	OY 721 AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGGGTAACACCTCCCCACGG 780 	OY 781 ATAGICTGCCTACCCTCAGGAATATTTTTGCTGTGGTACCTCAGCCTATCATTGTTG 840	OY 841 AATGGCTCTTCAGAATCTATGTGCTTCCTCTCTCTTTGTTGCCCCTATGACCATCTAC 900  B41 AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCTATGACCATCTAC 900	QY 901 ACTGAACAAGATTTATACAATCATGTGGTACCTAAGCCCCACAACAAAGAGTACCCATT 960 	QY 961 CTTCCTTTGTTATCAGAGGAGGAGGAGGAGCAGACTAGGCACTAGGCATTGCCAGTATC 1020

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RESULT 3
US-09-949-016-5640

j Sequence 6540, Application US/09949016

general information:
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    PRIOR APPLICATION NUMBER: 00/211,755
    PRIOR PLILING DATE: 2000-10-20
    PRIOR PLILING DATE: 2000-10-03
    PRIOR PLILING DATE: 2000-10-03
    PRIOR PLILING DATE: 2000-10-03
    PRIOR PLILING DATE: 2000-10-03
    PRIOR PLILING DATE: 2000-09-08
    NUMBER OF SEQ ID NOS: 207012
    SOFTHARE: PSELSEQ for Windows Version 4.0
    SEQ ID NO 5640
    LENGTH: 2763
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93.8%; Pred. No. 0;
:ive 0; Mismatches
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Matches 1389; Conserv
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; ORGANISM: Human
US-09-949-016-5640
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                                              GGAGCCACTGTCTGTTGGACTTACTTCACCCATACCAGTATGTCTGATGGGGGGTGGAATT
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                               CAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCAGGCCATACATTTCAATC
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                                                             CATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCC
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Sequence 21, Application US/09573080A

Sequence 21, Application US/09573080A

Patent No. 6828097

GENERAL INFORMATION:
APPLICANT: JOAN, KNOLL
APPLICANT: ROGAN, PETER
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF LING NUMBER: US/09/573,080A

CURRENT APLICATION WIMBER: US/09/573,080A

CURRENT FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 479

SEQ ID NO 21

LENGTH: 8523
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NAME/KEY: repeat region
LOCATION: (1)..(8523)
OTHER INFORMATION: herv17
PUBLICATION INFORMATION:
AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
TITLE: Proctotypic sequences for human repetitive DNA
JOURNAL: Journal of Molecular Evolution
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ilarity 93.8%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                | ISSUE: 4 | PAGES: 28-291 | DATES: 1992-10- | DATES: 1992-10- | DATABASE ACCESSION NUMBER: Database of | DATABASE ENTRY DATE: | DATABASE ENTRY DATE: | DATABASE ENTRY DATE: | 1996-01-26 | US-09-573-080A-21
                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
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Best Local Simil
Matches 1389; (
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	481 CATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCC 540	; GENERAL INFORMATION: ; APPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED THE OF INVENTION: WITH HIMAN DISEASE, WETHODS OF DETECTION AND USES THEREOF
	541 CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTTCAATC 600 	
	601 CCTGTTCCTGAACAATGGAACAACATCAGCACAGAAATAAACACCACTTCCGTTTTAGTA 660 	; PRIOR FILING DATE: 2000-10-20 ; PRIOR APPLICATION NUMBER: 60/237,768 ; PRIOR FILING DATE: 2000-10-03 ; PRIOR PLICATION NUMBER: 60/231,498
	661 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACTCACACCTGTGTAAAATTT 720 	
	721 AGCAATACTATAGACACAACCAGGCTCCCAATGCATCAGGTGGGTAACACCTCCCCACGA 780 	17508
	781 ATAGECTGCCTACCCTCAGGAATATTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTG 840 	Query Match Query Match Query Match Basel Local Similarity 93.8%; Pred. No. 0; Matches 1389: Conservative 0; Mismatches 92; Indels 0; Gaps 0;
` ^	841 AATGGCTCTTCAGAATCTATGTGCTTCCTCATTCTTAGTGCCCCCTATGACCATCTAC 900 	Angeccrcctratearactriccrrractor
<b>.</b> .	901 ACTGAACAAGATTTATACAATCATGTGCTACCTAAGCCCCACAACAAAGAGTACCCATT 960 	61
> 0	961 CTTCCTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC 1020 	121
<b>~</b> ^	1021 ACAACCTCTACTCAGTTCTACTACAACTATCTCAAGAAATAAAT	181
<b>&gt;</b> 0	1081 GTCACTGACTCCCTGGTCACCTTGCAACATCACTTAACTCCCTAGCAGCAGTAGTCCTT 1140 	241
<b>~</b> 0	1141 CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTATTTTA 1200 	301
<b>&gt;</b> 0	1201 GGAGAAGACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAA 1260 	361
<b>5</b> . 0	1261 ATTCGAGATCGAATACAATGTAGAGCAGGAGCTTCAAAACACCGAACGCTGGGGCCTC 1320 	421
<b>&gt;</b> .0	1321 CTCAGCCAATGGATGCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG 1380 	481
ъ <u>Р</u>	1381 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440 	541
> Q	1441 GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481 	601
ESULT S-09-9 Seque	SULT 5 -09-949-016-17382 Sequence 17382, Application US/09949016	Qy 661 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT 720 

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                                                                                              Gaps
                                                                  Length 145320
                                                                                              33;
                                                                                              IndelB
                                                                    DB 4;
                                                                                            81;
                                                                                                                           1 ATGGCCCTCCCTTATCATACTTTTCTCTTTACTGTTCTCT
                                                                  Score 1277.4;
Pred. No. 0;
0; Mismatches
                                                                  Query Match
Best Local Similarity 92.5%;
Matches 1399; Conservative
; LENGTH: 145320
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15858
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Patent No. 681239

GENERAL INFORMATION:
FAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: 00/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 15858
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                  ATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTC
                                                                                                                              ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCCACAACAAAAGAGTACCCATT
                                                                                                                                                                                    ACTGAACAAGATTTATACAGTTATGTCATATCTAAGCCCCGCAACAAAAGAGTACCCATT
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                                                                                                               AATGGCTCTTCAGAATCTATGTGCTTCCTCATTCTTAGTGCCCCCTATGACCATCTAC
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US-09-949-016-15858/c
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Pred. No. 2.4e-87;
0; Mismatches 25; Indels
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                                                                                        NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERRNCE/DOCKET NUMBER: WPB 39046A
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID NO: 108:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MCCOY, John
APPLICANT: MCCOY, John
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Pacie, David
APPLICANT: Treacy, Maurice
APPLICANT: Foans, Cheryl
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEIN
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/08686878A; Patent No. 5708157; GENERAL INFORMATION: APPLICANT: Jacobs, Kenneth
FILING DATE: 26-No. 65827
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1329 base pairs
                                                                                                                                                                                                                                                           TELEFAX: 703-836-2787 INFORMATION FOR SEQ ID NO: 108:
                                                                   ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.4%;
Best Local Similarity 92.7%;
Matches 317; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Massachusetts
COUNTRY: U.S.A.
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPBUTIC PURPOSES
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             TCTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTAT 1019
                                                                                                                                           1080 GGTCACTGCTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FRO PC COMPUTED
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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BESENE, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOWURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JEREMY
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 108, Application US/08979847B Patent No. 6582703 GENERAL INFORMATION:
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RESULT 10
US-09-99-016-184496/c

i Sequence 184496, Application US/09949016

patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WINHER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,768

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-09

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 184496
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Pred. No. 7.7e-42;
1; Mismatches 205; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AIGGCCCTCCCTTAICATACTTITCTCTTTACTGTTCTCTTACCCCC
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Pred. No. 7.7e-46;
0; Mismatches 17
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                         ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 849-8224
TELEPAX: (617) 846-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 542 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.9%;
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Best Local Similarity 91.5%;
Matches 184; Conservative C
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Best Local Similarity 60.23
Matches 320; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
US-08-721-489-2
                                                                                                                                                                                                                                                                                                                                                                                linear
      CLASSIFICATION:
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US-09-949-016-184496
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| Sequence 2, Application US/08721489
| Patent No. 5786465
| GENERAL INPORMATION:
| APPLICANT: McCOY, John
| APPLICANT: McCOY, John
| APPLICANT: Racie, Lisa
| APPLICANT: Treacy, Maurice
| APPLICANT: Racie, Lisa
| APPLICANT: Spaulding, Vikki
| TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
| TITLE OF INVENTION: ENCODING THEM
| NUMBER OF SEQUENCES: 5
| CORRESPONDENCE ADDRESS: ADDRESSE Genetics Institute, Inc.
| STREET: GambridgePark Drive CITY: CambridgePark Drive CITY: Cambridge STREET: No. 1 S has a stream of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of the comment of
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COMPUTER: IBM PC compatible
SOFTWARE: Patentln Release #1.0, Version #1.30
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,878A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BICANT. SOFT A.
REGISTRATION NUMBER: 32,724
TELEFORMUNICATION INFORMATION:
TELEFORM (617) 498-8224
TELEFORM: (617) 496-824
TELEFORM: (617) 876-5851
TELEFORM: (617) 876-5851
TELEFORM: CALARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/721,489
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 173.8; DB 1;
Pred. No. 7.7e-46;
0; Mismatches 17;
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Best Local Similarity 91.5%;
Matches 184; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
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ZIP: 02140
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Gaps

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Sequence 17025, Application US/09949016
; Sequence 17025, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
    APPLICANT: VEWTER, USCAPILISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT FILING DATE: 2000-04-14
; PRIOR RELING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PLING DATE: 2000-10-03
; PRIOR PELING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-01-03
; PRIOR FILING DATE: 2000-01-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10026
                                                                                                                                                                                                                                                                                                                                                                                       95871 TİCACCİAACİTCAGGCA--TİTİTİTİTCAİCİĞİĞAİTACACAĞGGİAİTGAİĞCCİA 95928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95929 AACAGCACTCTGAAGGAACTATGCTTTCACTCCTTTCTAGCACCTCCCATGTCCATATAT 95988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95989 actigaacaadactracaaagrerecrtraraceceaareregeeacaeardageerrrarr 96048
95635 GGTAATCCAACCAACTGCTGGATGTGTCTCCCCTTGCA-TTTTCAATGTATGTCCCAGTC 95693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95515 AGTACTCCCAGTCCATACAAGAAATTAGACCTTTCCAGGCTACAGGAAGCCCTTAACTCT
                                                                                                                                                                                                                                                                                         95811 AGCATGGCTGTCAATAAGAACACCTTCTGATGTCAGTCCTGTATATCAGTAACCCCAGGT
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                                                                                 95694 CCTGTCCCTGGACAGTGGAACTTATCCACCCCAGTACTAAACATCA---CCAAATCAATC
                                                                                                                                                                                       95751 AĞTCCCATAĞTCACCAATTTACCAGCCACAGGCCTCAAATCTCACGTGCATAAACTTC
                                                                                                                                                                                                                                             721 AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACAGA
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59.8%; Pred. No. 5.2e-40;
iive 0; Mismatches 212;
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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ORGANISM: Human
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Best Local S
Matches 324
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTENDN: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
GURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE FRACESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95515 AGTACTCCCAGTCCATACAAGAAATTAGACCTTTCCAGGCTACAGGAAGCCCTTAACTCT 95574
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                                                                                                                                                                                                                              661 GGACCICTIGITICCAAICIGGAAATAACCCAIACCICAAACCTCACCIGIGIAAAAITI
                                                                  GGTAATCCAACTGCTGGATGTGTCTCCCCTTGCA-TTTTCAATGTATGTCCCAGTC
                                                                                                                                  CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCCACTTCCGTTTTAGTA
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                                                                                                                                                                                                                                                                              AGTCCCATAGTCACCAATTTACCAGCCACACAGGCCTCAAATCTCACGTGCATAAACTTC
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                                      CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTCAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acreaaceaeaerracaaercrecrraraceceaarcreeceaeaear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12707, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)._.(190078); OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 59.8
Matches 324; Conservative
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LENGTH: 190078
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RESULT 14
US-09-949-016-202251
; Sequence 202251, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT. VEWTER, J. Craig et al.
APPLICANT. VEWTER, J. CLOUISOT
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CLOOUISOT
CURRENT APPLICATION NUMBER: 60/241, 755
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR PLILNG DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2000-10
; SUFTWARE: FREUSEZ for Windows Version 4.0
; SEQ ID NO 202251
LENTH: 601
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US-09-940-016-17417/C

JSGQUENCE 17417, Application US/09949016

REGION OF 681239

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17417
TYPE: DNA
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183 CTTCACTGCCCACCCATATGCCCCGCAACTGC 216
                                                477 TTTCACCATCCACACCCATATGCCCCTGCACTTC 510
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Pred. No. 2.5e-38;
0; Mismatches 32
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ilarity 84.6%;
Conservative
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Matches 181,
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| Sequence 202256. Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEWTER. VEW
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                                                                                                    CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA
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                                                                                                                                                                                                                     661 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTT
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Pred. No. 2.5e-38;
0; Mismatches 32;
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Best Local Similarity 84.6%;
Matches 181; Conservative C
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183 CTTCACTGCCCACACCCATATGCCCCGCAACTGC
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APPLICANT: Frederic BEDIN
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Glatte JOLIVET
APPLICANT: Bernard MANDRAND
TITLE OF INVENTION: VIRAL MATERIAL AND
TITLE OF INVENTION: THERAPEUTIC PURPOS
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REPERENCE/DOCKET NUMBER: WPB 38588
TELECOMMUNICATION:
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                               Sequence 58, Application US/08691563C Patent No. 6001987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 703-836-2787
INPORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1722 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleotide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Alexandria STATE: Virginia
                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Herve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILLE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: 06/241,755
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHWARE: FEATURE OF WINDOWS VETSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16147 ACCCCCCCCATGCCGCTATACTACCAGTAGCTCCCTTACCAAGAGCTTCTATGGAGAAT 16088
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                                                                                                                                                                                                                                                                                      16203 GGCCCCCCCCCCTCATATTTTTCTCTTTACTGTTGTCTTACCCCCCTTTCACTATCACCTC 16144
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                                                                                                                                                                                                                                                                                                                               ACCCCCTCCATGCTGCTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGAAC 122
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                                                                                                                                                                                                                                            GCCCTCCCTTATCATACTTTTCTCTTTACTGTTCTTTA-CCCCCTTTCGCTCTCACTGC
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                                                                                                                                                 Length 77772;
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Pred. No. 5.3e-37;
0; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 CITCACTGCCCACACCCATATGCCCCGCAACTGC 216
                                                                                                                                                        Score 150.8; DB Pred. No. 5.3e-37 0; Mismatches 3:
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Sequence 12249, Application US/09949016
Patent No. 6812339
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// OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12249
                                                               ; LOCATION: (1)...(77772)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17417
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84.6%;
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Best Local Similarity 84:68;
Matches 181; Conservative
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Best Local Similarity 84.6
Matches 181; Conservative
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NAME/KEY: misc_feature
                      FEATURE:
NAME/KEY: misc_feature
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      ORGANISM: Human
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LENGTH: 77997
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VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULITPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLAC
THERAPEUTIC PURPOSES
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9.8%; Score 145.6; DB 3; Length
Best Local Similarity 55.7%; Pred. No. 2.4e-36;
Matches 302; Conservative 0; Mismatches 234; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/691,563C FILING DATE: 02-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Oliff & Berridge
700 South Washington Street, Suite 300
16027 TTCACCATCCATATGCCCCTGCACTTC
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TUKE, PHILIP
TUKE, PHILIP
INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYI
THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1479
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                                                                                                                            940 CACAACAAAAGAGTACCCATTCTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTA
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                                                                          9
                        Length 1722;
                                                                          Indels
                        Score 145.6; DB 4;
Pred. No. 2.4e-36;
0; Mismatches 234;
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ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54, Application US/08979847B
Sequence 582703
GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
BESEME, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BEDIN, FREDERIC
PARANHOS-BACCALA, G
KOMURIAN-PRADEL, FI
JOLIVET-REYNAUD, CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 2320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MANDRAND, BERNARD
GARSON, JEREMY
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                        9.8%;
55.7%;
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                                                                                Conservative
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                                                       Similarity
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                                                       Best Local Sim
Matches 302;
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                              Query Match
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APPLICANT: Herve PERRON
APPLICANT: Frederic BEDIN
APPLICANT: Frederic BEDIN
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Glaucia PARANHOS-BACCALA
APPLICANT: Glatte JOLIVET
APPLICANT: Colette JOLIVET
APPLICANT: Bernard MANDRAND
TITLE OF INVENTION: HERAPEGITC PURPOSES
INVENTION: HERAPEGITC PURPOSES
TITLE OF INVENTION: HERAPEGITC PURPOSES
TITLE OF INVENTION: HERAPEGITC PURPOSES
TITLE OF INVENTION: HERAPEGITC PURPOSES
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
TITLE OF INVENTION: HERAPEGITC PURPOSES
TITLE OF INVENTION: HERAPEGITC PURPOSES
TITLE OF INVENTION: HERAPEGITC PURPOSES
TITLE OF INVENTION: HERAPEGITC PURPOSES
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
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REGISTRATION NUMBER: 30,024
REPERENCE/DOCKET NUMBER: WPB 38588
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 703-836-6400
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APPLICATION NUMBER: US/08/691,563
FILING DATE: 02-AUG-1996
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Patent No. 6579526
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LENGTH: 1722 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-374-766-58
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APPLICATION NUMBER: US
FILING DATE:
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COMPUTER: IBM PC compatible
COMPUTER: TBM PC.DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <un column column column column column column.
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NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
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ilarity 55.7%; Pred. No. 2.4
Conservative 0; Mismatches
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-08-979-8478-54
                                                                                                                                                                                                                                                                                              LENGTH: 1722 base pairs
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INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 302; Conserv
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RESULT 20 US-09-799-451-249 ; Sequence 249, Application US/09799451 ; Patent No. 6783969

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56.9%; Pred. No. 7.1e-36;
tive 0; Mismatches 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: PL_genes Version 2.0
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                                                                                                                                                                                                                                                                                           Zhao, Qing A.
Wang, Jian-Rui
Ma, Yunqing
Yamazaki, Victoria
Chen, Rui-hong
Goodrich, Ryle
Asundi, Vinod
Ren, Feiyan
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Xue, Aidong J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang, Zhiwei
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; LOCATION: (382
US-09-799-451-249
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Matches 286;
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APPLICANT: Frederic BESEME
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APPLICANT: Colette JOLIVET
APPLICANT: Colette JOLIVET
APPLICANT: Colette JOLIVET
APPLICANT: OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
TITLE OF INVENTION: THERAPEUTIC PURPOSES
OCRESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1036 ITCTACTACAAACTATCTCAAGAAATAAATGGTGACATGGAACAGGTCACTGACTCCCTG 1095
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1420 AAGTTTGTCTCTTCCAGAATTGAAGCTGAAAGCTACAGATGGTCTTACAAATGGAACCC
                         Gapa
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563C
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INPORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET UNMBER: WPB 38588
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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8.9%; Score 131.2; DB 3;
Best Local Similarity 57.6%; Pred. No. 1.2e-31;
Matches 257; Conservative 0; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oliff & Berridge 700 South Washington Street, Suite 300
                                                                                                                                                                                                                                               Sequence 46, Application US/08691563C
Patent No. 6001987
GENERAL INFORMATION:
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STRANDEDNESS: single
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US-08-691-563C-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A TITLE: Prototypic sequences for human repetitive DNA JOURNAL: Journal of Molecular Evolution VOLUME: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.6%; Score 142.4; DB 4; 55.4%; Pred. No. 7.2e-35;
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                                                                                                                                                                       APPLICANT: JOAN, KNOLL
APPLICANT: JOAN, KNOLL
APPLICANT: GOGAN, BETER
TITLE OF INVERTION: SINGLE COPY GENOMIC HYB
FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SOFTWARE: Patentin version 3.0
SOFTWARE: LENGTH: 8399
1925 TTCAGGCCATAAAGCTCCAGACG 1947
                                                                                                 Sequence 26, Application US/09573080A Patent No. 6828097 GENERAL INFORMATION:
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Best Local Similarity 55.4*
Matches 300; Conservative
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LOCATION: (1)...(8399)
OTHER INFORMATION: herv9
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAGES: 286-291
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                                                                                          US-09-573-080A-26
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPH)
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                                                                                                                                                                     1152 ctractroctadateccaaatagacterriggeadededegeretetedaaacegeeage
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                                           1036 TICTACTACAAACTATCTCAAGAAATAAATGGTGACATGGAACAGGTCACTGACTCCCTG
                                                                                                                                 1096 GTCACCTTGCAAGATCAACTTAACTCCCTAGCAGTAGTCCTTCAAAATCGAAGAGCT
                                                                                                                                                                                                                                                           1212 cradaccrecrederdadaaddaddacrerdeacerrerraadddaddarfi
                                                                                                                                                                                                                                                                                                                                                                                            1276 CAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTCCTCAGCCAATGGATG
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                                                                                   TTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTAGGAGAAGAACGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
9
  Indels
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  183;
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REPLICATION UNMERS: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <unknown>
  Mismatches
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NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42, Application US/08979847B Patent No. 6582703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARANHOS-BACCALA,
KOMURIAN-PRADEL, F
JOLIVET-REYNAUD, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MANDRAND, BERNARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: OLIFF & BERN
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PERRON, HERVE
BESEME, FREDERIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22320
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS
    Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BESEME,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-979-847B-42
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
THERAPEUTIC PURPOSES
      1216 TATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATA 1275
                                                                                            1276 CAATGTAGAGCAGAGGAGCTTCAAAACACGGAACGCTGGGGGCCTCCTCACCAATGGATG 1335
                                                                                                                                   1332 rcrgaaarcagacaacgccrrrcaaarrc----craraccaaccrcagagrrigggga 1385
                                                                                                                                                                                  1316 CCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTGTTACTCCTCTTTGGA 1395
                                                                                                                                                                                                                           1386 ACATGGTTTCTTCCTATGTCCCATGGCTGCCATCTTGCTATTACTCGCCTTTGGG 1445
                                                                                                                                                                                                                                                                      1396 CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTCCAGAATTGAAGCTGTAAAGCTA 1455
                                                                                                                                                                                                                                                                                                             1446 cecreratrirraacerectricreaaartricricricraecareagecereaagera 1505
                                                 1272 CTTTACACTAACCAGTCAGGGATAGTATGAGATGCTGCCGGCATTTACAGAAAAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.30
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Pred. No. 1.2e-31;
                                                                                                                                                                                                                                                                                                                                                            1456 CAGATGGTCTTACAAATGGAACCCCA 1481
                                                                                                                                                                                                                                                                                                                                                                                                     CAGATGGTCTTACAATGGAACCCCA 1531
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APPLICATION NUMBER: US/08/691,563
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Frederic BEDIN
Glaucia PARANHOS-BACCALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/374,766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Florence KOMURIAN-PRADEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46, Application US/09374766
Patent No. 6579526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Berridge, William P. REGISTRATION NUMBER: 30,02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Colette JOLIVET
APPLICANT: Bernard MANDRAND
TITLE OF INVENTION: VIRAL MA
TITLE OF INVENTION: THERAPEU
TITLE OF INVENTION: THERAPEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herve PERRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
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OPERATING SYSTEM:
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Best Local Similarity
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APPLICANT: Herve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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APPLICANT:
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951 AGTACCCATTCTTCTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCAT 1010
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APPLICANT: CALVERT, JAY G.
APPLICANT: CALVERT, JAY G.
APPLICANT: WITTER, RICHARD L.
APPLICANT: WIANGIDA, NOBORU
TITLE OF INVENTION: VACCINE COMPRISING FOWLPOX VIRUS
TITLE OF INVENTION: RECOMBINANTS EXPRESSING THE ENVELOPE GLYCOPROTEIN OF
TITLE OF INVENTION: AVIAN RETICULOENDOTHELIOSIS RETROVIRUS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                         NAME/KEY: misc binding

LOCATION: 484...502

OTHER INFORMATION: 12-5-158.misl

NAME/KEY: misc binding

LOCATION: 684...503

OTHER INFORMATION: 12-5-158.mis2, potential complement

NAME/KEY: primer bind

LOCATION: 346...366

OTHER INFORMATION: upstream amplification primer

NAME/KEY: primer bind

COTHER INFORMATION: downstream amplification primer, complement

NAME/KEY: misc binding

LOCATION: 491...515

OTHER INFORMATION: 12-5-158 potential probe

NAME/KEY: misc feature

LOCATION: 314...336, 793

COTHER INFORMATION: n=a, g, c or t

US-09-671-317-406
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                                                                                                                                   LOCATION: 503
OTHER INFORMATION: 12-5-158 : polymorphic base C or
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Pred. No. 1.8e-31;
0; Mismatches 99;
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8110 Gatehouse Road Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08007282B
Patent No. 5403582
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 67.6%;
Matches 211; Conservative
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                                               TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                NAME/KEY: allele
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US-08-007-282B-1
SEO ID NO 406
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| Sequence 406, Application US/09671317
| Patent No. 6528260
| GENERAL INFORMATION:
| APPLICANT: Blumenfeld, Marta
| APPLICANT: Blumency, Ilya
| APPLICANT: Chumakov, Ilya
| APPLICANT: Chumakov, Ilya
| APPLICANT: Cohen, Annick
| TITLE OP INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
| TITLE OP INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
| TITLE OP INVENTION: BIALLELIC MARKERS PORTON OF 2.03.CIP
| CURRENT APPLICATION NUMBER: US 09/536,178
| PRIOR FILING DATE: 2000-03-23
| PRIOR PILING DATE: 2000-03-24
| PRIOR APPLICATION NUMBER: US 60/126,269
| PRIOR PILING DATE: 1999-03-25
| PRIOR FILING DATE: 1999-03-25
| PRIOR FILING DATE: 1999-04-30
| NUMBER OF SEQ ID NOS: 977
| WUMBER OF SEQ ID NOS: 977
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Pred. No. 1.2e-31;
0; Mismatches 183;
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                       TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1859 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPPOLOCY: linear
MOLECULE TYPE: cDNA
       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                      Query Match 8.9%;
Best Local Similarity 57.6%;
Matches 257; Conservative (
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Sequence 14685, Application US/09949016

Sequence 14685, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949, 016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231, 768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

NUMBER OF SEQ ID NOS: 207012
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Sequence 184497, Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        997 CTAGGTACTGGCATTGGCAGTATCACAACCTCTACTACTACAAAACTATCTCAA 1056
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Pred. No. 2.8e-26;
0; Mismatches 217; Indels
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Best Local Similarity 54.2%;
Matches 260; Conservative
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ORGANISM: Human
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LENGTH: 21526
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                                                                                                                                                                                        COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,282B
FILING DATE: 19330121
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WURPHY JR., GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1644-104P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 103-205-8000
TELEFAX: 703-205-8050
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                                                                                                                                                                             3: Floppy disk
IBM PC compatible
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
Falls Church
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                                                                       COUNTRY:
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                                                                                                                                                                                                                                                         Length 7713;
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                7.8%; Score 115.2; DB 4;
54.0%; Pred. No. 5e-26;
tive 0; Mismatches 218;
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US-09-573-080A-44
; Sequence 44, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL
; APPLICANT: ROGAN, PETER
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBE
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/573,080A
; CURRENT FILING DATE: 2000-05-16
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SOFTWARE: Patentin version 3.0
SEQ ID NO 44
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Best Local Similarity 54.0
Matches 259; Conservative
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LOCATION: (1)..(7392)
OTHER INFORMATION: hervr
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
  PUBLICATION INFORMATION
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US-09-573-080A-30
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APPLICANT: GOAN, ETER
TITLE OF INVENTION: BTER
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATI
FILE REPERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SSCTIPMARE: PALENTIN VERSION 3.0
LENGTH: 7713
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Pred. No. 3.5e-27;
1; Mismatches 175;
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 184497
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GENERAL INFORMATION:
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Best Local Similarity 58.55
Matches 257; Conservative
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: repeat_region
LOCATION: (1). (7713)
OTHER INFORMATION:
PUBLICATION INFORMATION:
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                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
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US-09-573-080A-30
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                      AGCACCCCTAGCCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCTCCGTACC
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Pred. No. 2.9e-25;
0; Mismatches 202;
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APPLICANT: Du Sart, Desiree
APPLICANT: Du Sart, Desiree
APPLICANT: Du Sart, Desiree
APPLICANT: Du Sart, Desiree
FILE REPERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER: OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 55.7'
Matches 263; Conservative
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LENGTH: 80246
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                                                                                                                              ISSUE: 4
PAGES: 286-291
DATE: 1992-10-
DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
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JETLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILL OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND UPILE REFERENCE: CLOO130.

CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILLING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR PALLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-09
PRIOR FILLING DATE: 2000-09-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 160; Indels
AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A TITLE: Prototypic sequences for human repetitive DNA JOURNAL: Journal of Molecular Evolution
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Pred. No. 1.4e-26;
1; Mismatches 128;
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Pred. No. 5.6e-26;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6812339
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Best Local Similarity 56.9%;
Matches 211; Conservative (
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Best Local Similarity 61.8
Matches 215; Conservative
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GAPLICANT: Collins, Mary KL
APPLICANT: Collins, Mary KL
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
BARLIER APPLICATION NUMBER: GB9517263.1
EARLIER PILING DATE: 1995-08-23
EARLIER FILING DATE: 1995-08-23
SOFTWARE: PATENTIN UNCE: 2.0
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1165 CIBACCGCCBABAGAGGGGBACCTGTTTTTBGGAGAGGAGCGCTGTTATTATGTT 1224
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Pred. No. 8.8e-26;
0; Mismatches 183;
Sequence 8, Application US/09011745; Sequence 8, Application US/09011745; Patent No. 6165715; GENERAL INFORMATION:
APPLICANT: Collins, Mary KL; APPLICANT: Weise, Robin A.; APPLICANT: Weise, Robin A.; APPLICANT: Cosset, Francois-Loic; TITLE OF INVENTION: Expression systems; FILE REFERENCE: 09/011,745; CURRENT APPLICATION NUMBER: US/09/011,745; CURRENT FILING DATE: 1998-08-23; EARLIER PILING DATE: 1996-08-23; EARLIER PILING DATE: 1995-08-23; NUMBER OF SEQ ID NOS: 29; SOFTWARE: PatentIn Ver. 2.0; SEQ ID NO 8: 20.
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LOCATION: (3802)
SOTHER INFORMATION: n is any nucleotide
US-09-011-745-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (361<u>T)</u>
OTHER INFORMATION: n is any nucleotide
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Best Local Similarity 55.0%;
Matches 224; Conservative (
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                                                                                                                                                                            AATCCAGAATTGTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGCAG 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTGTTACTCCTCTTTGGACCCTGTA 1402
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                                                                                                      6078 cagcgaaaaaccacaacrcriccririrircracaacacacrarriccriraacc
                                                                                                                                                                                                                                                                                                                                             AGGAGCTTCAAAACACCGGAACGCTGGGGCCTC-----CTCAGCCAATGGATGCCTGGG
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                                                                                                                                                                                                                                                               6138 AATCTGGCGTGATACAGGATACTGTAAAAAGACTAAAGGACCGAGCACAAAAATTAAAG
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Patent No. 654479

GENERAL INFORMATION:

APPLICANT: Cichutek, Klaus

APPLICANT: Cichutek, Klaus

TITLE OF INVENTION: PSEUDO-TYPE RETROVIRAL VECTORS WITH

TITLE OF INVENTION: MODIFIABLE SURFACE CAPSID PROTEINS

TILLE REFERENCE: 11692-005601

CURRENT APPLICATION NUMBER: US/09/555,352

CURRENT APPLICATION NUMBER: PCT/DE98/03542

PRIOR PILING DATE: 1998-11-27

PRIOR FILING DATE: 1998-11-28

NUMBER OF SEQ ID NOS: 34

NUMBER OF SEQ ID NOS: 34
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Pred. No. 3.5e-25;
0; Mismatches 243;
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ORGANISM: Murine leukemia virus
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258; Conservative
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Best Local S:
Matches 258
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CTAACGGCAGAACAAGGAGGAATTTGTTTAGCCTTACAAGAAAAATGCTGTTTTTATGCT 2871
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Pred. No. 3.1e-25;
0; Mismatches 224; Indels
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Patent No. 6828097
GENERAL INFORMATION:
APPLICANT: JOAN, KNOLL
APPLICANT: ROGAN, PETER
TITLE OF INVENTION: SINGLE COPY GENOMIC HYB
FILE REFERENCE: 33307
CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
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US-09-573-080A-28
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US-09-573-080A-28
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Pred. No. 5.7e-23;
0; Mismatches 187;
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TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PO2032D1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
PRIOR PELICATION NUMBER: 09/511,554
PRIOR FILING DATE: 2000-02-23
PRIOR PELICATION NUMBER: 60/097,917
PRIOR PELICATION NUMBER: 60/099,634
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PATCHIN VOY: 2.0
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Best Local Similarity 54.8%;
Matches 230; Conservative
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                                                       CIGGGGCCTCCTCAGCCAATGCATGCCCTGGGTTCTCCCCTTTAGGACCTCTAGCAGC 1370
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                                                                                                    1371 TCTAATATTGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTC
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ITLE OF INVENTION: No. 6569662el Nucleic Acids and
ITLE OF INVENTION: Polypebtides
ITLE REPERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL_genes Version 1.0
SEQ ID NO 17-1
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7.2%; Score 106.4; DB 4;
Best Local Similarity 55.0%; Pred. No. 1.9e-23;
Matches 231; Conservative 0; Mismatches 186;
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Patent No. 6569662
GENERAL INFORMATION:
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Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Chen, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Yian-Rui
APPLICANT: Zhou, Ping
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; LOCATION: (1936)..(2364)
US-09-620-312D-171
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US-09-620-312D-171
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                                     GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307

CORRENT APPLICATION NUMBER: 08/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR RILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASCES OF Windows Version 4.0
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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Pred. No. 1.5e-21;
0; Mismatches 211; Indels
Sequence 12735, Application US/09949016
Patent No. 6812339
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16; Conservative
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US-09-949-016-13572/c
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; ORGANISM: Human
US-09-949-016-12735
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LENGTH: 80355
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Matches 246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Score 103.4; DB 4;
Pred. No. 1.5e-21;
0; Mismatches 211;
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SQCIPMARE: FBSEG for Windows Version 4.0
SQCIPMARE: 80357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: February 21, 2005, 15:01:25 Job time : 267.948 secs
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ilarity 53.1%;
Conservative
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Matches 246; Conserv
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US-09-949-016-13572
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US-08-979-847-105
                                                                                                                                                                                                                                     (without alignments)
10694.149 Million cell updates/sec
                                                                                                                                                                                                 February 21, 2005, 11:52:50 ; Search time 818.526 Seconds
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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22: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 105, App	Sequence 105, App	Sequence 18, Appl	Sequence 4, Appli	Sequence 1, Appli	Sequence 134, App	Sequence 3, Appli	Sequence 3, Appli	Sequence 21, Appl	Sequence 81, Appl	Sequence 30, Appl
ΩI	8 US-08-979-847-105	US-10-114-104-105	US-10-637-565-18	US-10-416-642-4	US-09-902-535-1	US-10-114-893-134	US-10-016-249-3	US-10-133-036-3	US-09-854-867-21	US-09-873-367C-81	US-10-632-793-30
DB	8	16	17	17	σ	13	15	17	10	10	17
% Query e Match Length DB I	1481	1481	2030	2074	2930	2946	2946	1617	8523	56093	7582
% Query Match	100.0	100.0	100.0	93.8	90.2	90.2	90.2	90.1	90.1	90.1	89.4
Score	1481	1481	1481	1389.8	1335.4	1335.4	1335.4	1333.8	1333.8	1333.8	1324.2
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1, 7	Ñ	e 730,	4444	Seguence 24, Appl	21192	e 22	19,	25	23	Sequence 322491,		Sequence 322491,		Sequence 4312, Ap					O1	~	Sequence 108, App				Sequence 86541, A	Sequence 86541, A		ø	~	Sequence 150080,		Φ.	Sequence 85218, A
	7 US-10-632-793-26		US-09-864-761-4444	7 US-10-632-793-24	US-09-864-761-21192	7 US-10-363-616-228	7 US-10-632-793-19	7 US-10-632-793-25	7 US-10-632-793-23		3 US-10-027-632-322492		7 US-10-027-632-322492	6 US-10-029-386-4312	3 US-10-027-632-322574	3 US-10-027-632-322575	7 US-10-027-632-322574	7 US-10-027-632-322575	7 US-10-292-798-1393	US-08-979-847-108	6 US-10-114-104-108	US-09-864-761-14030	3 US-10-027-632-316412	7 US-10-027-632-316412	3 US-10-027-632-86541		US-09-864-761-7501	6 US-10-029-386-20259	US-09-864-761-7310	3 US-10-027-632-150080	7	-027-632-8	7 US-10-027-632-85218
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## ALIGNMENTS

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Publication US/08979847
Publication US/0803039664A1
Publication US/0803039664A1
Sequence 105. Application US/0803039664A1
SEDENEAL INPORMATION:
APPLICANT: BESEME, FREDERIC
APPLICANT: BESEME, FLORENCE
APPLICANT: BESEME, FLORENCE
APPLICANT: WANDRAND. BERNARD. COLETTE
APPLICANT: WANDRAND. BERNARD
APPLICANT: WANDRAND. BERNARD
APPLICANT: WANDRAND. BERNARD
APPLICANT: WANDRAND. BERNARD
APPLICANT: WANDRAND. BERNARD
APPLICANT: WANDRAND. BERNARD
APPLICANT: WANDRAND. BERNARD
APPLICANT: WASCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLAC
TITLE OF INVENTION: THERAPEUTIC PURPOSES
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSE: OLIFF & BERRIDGE, PLC
STREET: D. GOX 19928
CITY: ALEXANDRIA
STREET: NA
COUNTRY: USA
CONFUTER READBLE FORM:
MEDIUM TYPE: PLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEATHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLING DATE: 26-NOV-1997
CLASSIFICATION: 435
CLASSIFICATION: 435
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TUKE, PHILIP
TUKE, PHILIP
OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYI
THERAPEUTIC PURPOSES
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AATGGCTCTTCAGAATCTATGTGCTTCCTCATTCTTAGTGCCCCCTATGACCATCTAC
                                                     ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCCACAACAAAAGAGTACCCATT
                                                                                                     CTTCCTTTTGTTATCAGAGCAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STRATE: VA
COUNTRY: USA
ZIP: 22320
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BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JEREM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 105, Application US/10114104 Publication No. US20030198647A1 GENERAL INFORMATION:
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                                              39046A
     ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WB 390
TELECOMMUNICATION INFORMATION:
TELECHNE: 703-83-2787
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 base pairs
TYPE: nucleic acid
STRANDEDNESS: 81ngle
TYPE: TOPOLOGY: linear
NOLECULE TYPE: CDNA
                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 1481; Conservative 0;
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RESULT 3

US-10-637-565-18

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US-10-637-565-18

Spiciant on No. US20040043381A1

GENERAL INFORMATION:

APPLICANT: PARANHOS-BACCALA, Glaucia:

APPLICANT: KOMURIAN-PRADEL, Florence

APPLICANT: KOMURIAN-PRADEL, Florence

TITLE OF INVENTION: THE LIR REGION OF MSRV-1 AND THE PROTEINS IT ENCODES, AND PROBES

TITLE OF INVENTION: METHODS FOR DETECTING MSRV-1 RETROVIRUS

FILE REPERENCE: 110257

CURRENT APPLICATION NUMBER: US/10/637,565
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NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEPRAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 105:
     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,104
FILING DATE: 03-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1481;
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-114-104-105
                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,847
FILING DATE: 26-NOV-1997
                                                                                                                                                                                                                                                                      LENGTH: 1481 base pairs
                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 1481; Conservative
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ORGANISM: Homo sapiens
PEATURE:
OMAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040043452A1 7477736CB1
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Publication No. US20040043452A1

GENERAL INPORMATION:

APPLICANT: INCYTE GENOMICS, INC.

APPLICANT: RAMKUMAR, JAyalaxmi

APPLICANT: RAMKUMAR, JAyalaxmi

APPLICANT: APPLICANT: PF-0842 PCT

CURRENT APPLICATION NUMBER: US/10/416,642

CURRENT FILING DATE: 2003-05-13

PRIOR FILING DATE: 2003-05-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PERL PROGRAM

SOFTWARE: PERL PROGRAM

SOFTWARE: PERL PROGRAM

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SOFTWARE: PERL PROGRAM
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US/09/890,340
PRIOR FILING DATE: 2001-11-27
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 1999-02-15
PRIOR FILING DATE: 1999-02-15
NUMBER OF SEQ ID NOS: 20
SEQ ID NOS: 20
SEQ ID NOS: 20
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Best Local Similarity 100.0%;
Matches 1481; Conservative 0
                                                                                                                                                               TYPE: DNA ORGANISM: MSRV-1 retrovirus
                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (1)..(1626)
US-10-637-565-18
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ilarity 93.9%;
Conservative (
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; LOCATION: (930)...(2546)
US-09-902-535-1
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ORGANISM: Homo sapiens
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Best Local Simi
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                                                                0; Gaps
                                               Length 2074;
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                                                DB 17;
                                                Score 1389.8;
Pred. No. 0;
0; Mismatches
                          or other
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                                               Query Match

Best Local Similarity 96.2%;
Matches 1424; Conservative
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; FEATURE:
; NAME/KES:
; LOCATION: 1995
; OTHER INFORMATION: a, t,
US-10-416-642-4
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	RESULT 6 US-10-114-893-134 Sequence 194, Application US/10114893 Sequence 194, Application US/10114893 Publication No. USZ0020193567A1 GENERAL INFORMATION: APPLICANT: GACOY, OND M. APPLICANT: Colline-Racie, Lisa A. APPLICANT: Colline-Racie, Lisa A. APPLICANT: Caraba, Cheryl APPLICANT: Treacy, Maurice APPLICANT: Treacy, Maurice APPLICANT: Spaulding, Vikki APPLICANT: Spaulding, Vikki APPLICANT: Garlin-Duckett, McKeough APPLICANT: Garlin-Duckett, McKeough APPLICANT: Garlin-Duckett, Inc. APPLICANT: Garlin-Duckett, McKeough APPLICANT: Garlin-Duckett, McKeough APPLICANT: Garlin-Duckett, McKeough APPLICANT: Garlin-Duckett, McKeough APPLICANT: Garlin-Duckett, McKeough APPLICANT: Garlin-Duckett, McCeough APPLICANT	Ouery Match  Best Local Similarity 93.9%; Pred. No. 0,  Matches 1390, Conservative 0; Mismatches 91; Indels 0; Gaps 0;  Matches 1390, Conservative 0; Mismatches 91; Indels 0; Gaps 0;  Oy 1 ATGGCCTCCCTTATCTTTTTCTTTACTGTTCTTTACCCTTTCGCTCTCACT 60  S28 ATGGCCTCCCTTATCATTTTTCTTTTACTGTTCTTTTCACTCTTCACT 987  Oy 61 GCACCCCTCCATGCTGCTGCTACAACCTCTTTACCCTTTCACTCAC
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CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTTCAATC
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                                                          APPLICANT: Conrad, Bernard
APPLICANT: Conrad, Bernard
TITLE OF INVENTION: Multiple Sclerosis-Related Superantigen
FILE REFERENCE: 23135-507
CURRENT APPLICATION NUMBER: US/10/133,036
CURRENT APPLICATION NUMBER: EV7/EP00/10659
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3.
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                             ORGANISM: Human endogenous retrovirus
                    Sequence 3, Application US/10133036; Publication No. US20040054133A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   90.1%;
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Best Local Similarity 93.8
Matches 1389; Conservative
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                                                Query Match
90.1%; Score 1333.8;
Best Local Similarity 93.8%; Pred. No. 0;
Matches 1389; Conservative 0; Mismatches
; LOCATION: (1)..(8523)
; OTHER INFORMATION: hervl7
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APPLICANT: JOAN, KNOLL H
APPLICANT: SOGAN, PETER K
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/854,867
CURRENT FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 613
SOFTWARE: Patentin version 3.1
SEQ ID NO 21
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Publication No. US20030224356A1
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ORGANISM: Homo sapiens
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                  GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
                                                      GTCGCCGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT
                                                                      CAAAATCGAAGACTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA
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90.1%; Score 1333.8;
Best Local Similarity 93.8%; Pred. No. 0;
Matches 1389; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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ATGGCCTCCCTTATCATATTTTTCTCTTTACTGTTCTTTTACCCTCTTTCACTCTCACT
                                                                                        ACGOGGCTTCCTGGAAATATTGATGCCCCATCATATAGGAGTTTATCTAAGGGAAACTCC
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NAME/KEY: misc feature
LOCATION: (4115). (4115)
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Best Local Similarity 92.2%
Matches 1365; Conservative
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NAME/KEY: misc_feature
LOCATION: (3787)..(3787)
OTHER INFORMATION: n = a
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NAME/KEY: misc_feature
LOCATION: (2398)
OTHER INFORMATION: n = a
             LOCATION: (2213)..(2213)
OTHER INFORMATION: n = a
NAME/KEY: misc feature
LOCATION: (2213) .. (221)
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Sequence 30, Application US/10632793

Publication No US20040048298A1

GENERAL INPORMATION:
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: VOISSET, Cecile
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN FILE REFERENCE: 110048

CURRENT APPLICATION NUMBER: US/10/632,793

CURRENT FILING DATE: 2001-10-22

PRIOR APPLICATION NUMBER: PCT/FR00/00144

PRIOR APPLICATION NUMBER: FR 99/00888

PRIOR APPLICATION NUMBER: FR 99/00888

PRIOR APPLICATION NUMBER: FR 99/00888

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 30

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                              1261 ATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTC
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NAME/KEY: misc feature
LOCATION: (1331). (1331)
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NAME/KEY: misc_feature
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OTHER INFORMATION: n = a.
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       ATAGTCTGCCTACCCTCAGGAATATTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTG
                                     AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTAC
                                                                                        ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCACAAAAGAGTACCCATT
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; Beneral Inroparation No. US2004005413341
; GENERAL INPORMATION:
; APPLICANT: Concad, Bernard
; APPLICANT: Mach, Bernard
; TITLE OF INVENTION: Multiple Sclerosis-Related Superantigen
; FILE REFERENCE: 23135-507
; CURRENT APPLICATION NUMBER: US/10/133,036
; CURRENT APPLICATION NUMBER: PCT/EP00/10659
; PRIOR PLING DATE: 2002-04-26
; PRIOR PLING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 1
; LENGTH: 2782
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; ORGANIEM: Human endogenous retrovirus
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Length
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Score 1308.2;
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  Query Match
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Matches 1373; Conservative
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	ACCTTCACTGCCCACACCCATAIGCCCCGCAACTGCTATCACTTGCCTGTGCACTCTTTGCATG 10				421 AGCACCCTAGCCCCTACAAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCGGTACC 480	481 CATACTCGCCTGGTGAGCCTATTTAATACCACCTCACTCGGCTCCATGAGGTCTCAGCC 540	541 CAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCAGGCCATACATTTCAATC 600	601 CCTGTTCCTGAACAATGGAACATTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA 660 	661 GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAATTT 720 	721 AGGAATACTATAGACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACACGA 780	781 ATAGICIGCETACCETCAGGAAIATITITIGICIGIGGIACCECAGCCIAICATIGITIG 840	841 AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTAC 900	901 ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCACAACAAAGAGTACCCATT 960 	961 CTTCCTTTTGTTATCAGAGGAGGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATC 1020	1021 ACAACCTCTACTCTACTACTACAAACTATCTCAAGAAATAAAT	1081 GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT 1140 	1141 CAAAATCGAAGGTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA 1200 	1201 GGAGAAGGACGCTGTTATTATGATGAGAATTGTCACTGAGAAAGTTAAAGAA 1260 
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Best Local Similarity 92.5%;
Matches 1399; Conservative
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EXPRESSED IN BRAIN, SIGNAL = 6.2
EXPRESSED IN BONE MARROW, SIGNAL
EXPRESSED IN LUNG, SIGNAL = 3.9
EXPRESSED IN HELA, SIGNAL = 7.2
                                                                                                                    Query Match 76.4%; Score 1131.6; DB 9; Best Local Similarity 92.4%; Pred. No. 0; Matches 1218; Conservative 0; Mismatches 84;
 ; OTHER INFORMATION: E; OTHER INFORMATION: E; OTHER INFORMATION: E; OTHER INFORMATION: E; OTHER INFORMATION: E
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Sequence 4444, Application US/09664761

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ORGANISM: Homo sapiens
PEATURE:
OTHER INFORMATION: MAP TO AC002346.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN HEALTO, SIGNAL = 6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.4
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 5.9
                                                                                                                   AAATGGAACCCCA 1481
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Sequence 24, Application US/1063293

Publication No. US20040048298A1

GENERAL INFORMATION:
APPLICANT: PRARNHOS-BACCALA, Glaucia
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: WALLET, Francois
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
FILE REFREENCE: 110048
CURRENT APPLICATION NUMBER: US/09/869,927

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 1999-01-21

PRIOR FILING DATE: 1999-01-21

SEQIIO NOS: 33

SOFTWARE: PACENTIN VERSION 3.1

SEQIIO NO 24

SEQIIO NO 24

LENGTH. 10.48
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; LOCATION: (241)
; OTHER INFORMATION: n = a or g us.
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LOCATION: (84)...(84)
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EXPRESSED IN BRAIN, SIGNAL = 6.2
EXPRESSED IN BONE MARROW, SIGNAL = 6.3
EXPRESSED IN LUNG, SIGNAL = 3.9
EXPRESSED IN HELA, SIGNAL = 7.2
MT HIT: AF208161.1, EVALUE 0.00e+00
EST HUMAN HIT: AU138405.1, EVALUE 0.00e+00
SWISSPROT HIT: P10269, EVALUE 2.00e-16
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US-10-363-616-228
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APPLICANTY HARRY BARK, David R.
APPLICANTY HARRY DAVID R.
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APPLICANTY HARRY DAVID REBERGE STON ANALYSIS BY MICROARRAY
FILE REPERENCE: Accordica.X-11
CURRENT PALLICATION WUMBER: US 60/180,312
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-20
PRIOR APPLICATION WUMBER: US 60/207,456
PRIOR PLING DATE: 2000-06-03
PRIOR PLING DATE: 2000-06-03
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ORGANIZM: Homo sapiens
ORGANIZM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 20
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Patent No. US20020048763A1
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Best Local Similarity 98.8%; Pred. No. 6.2e-171;
Matches 596; Conservative 0; Mismatches 7; Indels 0;
                                   POLYPEPTIDES
FUBLICATION NO. US20040044181A1
GENERAL INFORMATION:
APPLICANT: Hyeeq. Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POL.
FILE REFERENCE: 21272-113 (793)
CURRENT FILING DATE: 2003-03-03
FRIOR APPLICATION NUMBER: 09/654,935
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
SEQ ID NO 228
LENGTH: 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 19
US-10-632-793-19
IS-10-632-793-19
; Sequence 19, Application US/10632793
; Publication No. US20040048298A1
; GENERAL INFORMATION:
                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                       ) NAME/KEY: CDS
; LOCATION: (89)..(1684)
US-10-363-616-228
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APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: MALLET, Francois
APPLICANT: WALLET, Francois
APPLICANT: VOISSET. Cecile
TITLE OF INVENTION: ENDOGRENCOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
FILE REFERENCE: 110048
CURRENT PAPLICATION NUMBER: US/09/869,927
PRIOR ENTOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: PCT/FR00/00144
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 1999-01-21
PRIOR FILING DATE: 1999-01-21
PRIOR FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SOCIATION NUMBER: PCT/FR00/0144
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Pred. No. 2e-168;
0; Mismatches 2; Indels
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; Sequence 25, Application US/10632793
; Publication No. US20040048298A1
; PUBLICATION:
; APPLICANT: PARANHOS-BACCALA, Glaucia
                                                                                                                                                                                                                                                                                                                                                                                                                                          39.4%;
99.7%;
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Matches 584; Conservative
                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-632-793-19
                                                                                                                                                                                                                                                                                                                           SEQ ID NO 19
LENGTH: 591
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FEATURE
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APPLICANT: MALLET, Francois
APPLICANT: VOISSET, Cecile
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMUB DISEASE, LABELING METHOD AND REAGENT
FILE REFERENCE: 110048
CURRENT APPLICATION NUMBER: US/10/632,793
CURRENT PILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US/09/869,927
PRIOR FILING DATE: 2000-10-22
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
ESC ID NO 25
LENGTH: 1136
THE REFERENCE TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO 
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Pred. No. 7.5e-148;
0; Mismatches 49;
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Best Local Similarity 91.8%;
Matches 546; Conservative (
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US-10-632-793-25
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Sequence 23, Application US/10632793
Publication No. US20040048298A1
GENERAL INFORMATION:
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: MALLET, Francois

US-10-632-793-23

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APPLICANT: VOISSET, Cecile
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
FILE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
FILE REFERENCE: 110048
CURRENT APPLICATION NUMBER: US/10/632,793
CURRENT APPLICATION NUMBER: US/09/869,927
PRIOR APPLICATION NUMBER: US/09/869,927
PRIOR APPLICATION NUMBER: PC/FR00/00144
PRIOR PILING DATE: 2000-1.21
PRIOR PELING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 23
LENGTH: 2006
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Pred. No. 8.6e-147;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature

) LOCATION: (305)..(305)

) OTHER INFORMATION: n = a or g or c or t/u

US-10-632-793-23
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US-10-027-632-322491/c
Sequence 322491, Application US/10027632
Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 93.2%;
Matches 548; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Human
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SEQ ID NO 322492
LENGTH: 570
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GUREALL INFORTATION:

GREAL INFORTATION:

GREAL INFORTATION:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-07-29

PRIOR PILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PILING DATE: 1099-11-28

PRIOR PILING DATE: 1099-104-28

PRIOR FILING DATE: 1099-104-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-38

PRIOR FILING DATE: 1999-09-38

PRIOR FILING DATE: 1999-09-38

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

SOFTWARE: FASTERQ ID NOS: 325720

SOFTWARE: FASTERQ FOR Windows Version 4.0

LENGTH: 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.5%; Score 377.8; DB 13; Length Best Local Similarity 90.7%; Pred. No. 3e-105; Matches 411; Conservative 2; Mismatches 39; Indels
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US-10-027-632-322491
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)...(570)
                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FITLE OF INVENTION: Identification in the Human Genome
FILE REPERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2000-07-12
FRIOR PAPLICATION NUMBER: US 60/198,676
FRIOR PAPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR PAPLICATION NUMBER: US 60/167,363
FRIOR FILING DATE: 2000-02-29
FRIOR FILING DATE: 1909-01-23
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR APPLICATION NUMBER: US 60/166,358
FRIOR APPLICATION NUMBER: US 60/166,358
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
FRIOR FILING DATE: INDOME VERSION 4.0
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Pred. No. 3e-105;
2; Mismatches 39; Indels 1;
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| LOCATION: (1)...(570)
| OTHER INFORMATION: n = A,T,C or G
| US-10-027-632-322492
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Best Local Similarity 90.7
Matches 411; Conservative
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RESULT 24 US-10-027-632-322491/c

RESULT 23 US-10-027-632-322492/c ; Sequence 322492, Application US/10027632

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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
RIOR FILING DATE: 2000-07-12
RIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-22
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-02-28
PRIOR PELING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
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Sequence 322491, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:

', LOCATION: (1)...(570)

', OTHER INFORMATION: n = A,T,C or G
US-10-027-632-322491

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Best Local Similarity 90.7
Matches 411; Conservative
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LENGTH: 570
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JAPPICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REPERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-07-12

PRIOR PAPLICATION NUMBER: US 60/193,483

PRIOR PAPLICATION NUMBER: US 60/193,483

PRIOR PILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08-09

PRIOR FILING DATE: 1999-08-09
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Pred. No. 3e-105;
2; Mismatches 39; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 322492
LENGTH: 570
Sequence 322492, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or
US-10-027-632-322492
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Best Local Similarity 90.7%;
Matches 411; Conservative
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
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23.8%; Score 353; DB 13; Length 551;
Best Local Similarity 92.0%; Pred. No. 1.3e-97;
Matches 412; Conservative 2; Mismatches 30; Indels 4
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
SOFTWARE: FASTERO FOR WINDOWS VERSION 4.0
SEQ ID NOS: 325720
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; Publication No. US20020198371A1
; GENERAL INFORMATION:
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US-10-027-632-322574
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LOCATION: (1)...(551)
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ORGANISM: Human
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                                             Sequence 4312, Application US/10029386
Sequence 4312, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
BAPLICANT: Penn, Sharron G.
APPLICANT: Penn, Bavid R.
APPLICANT: Hanzel, David R.
APPLICANT: HARZEl, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CITLE REFERENCE: AEDMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOUTHWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 4312
LENGTH: 521
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221 TCTAGCGACTATAATACTGTTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTTTAA
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
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OTHER INFORMATION: MAP TO ACO21619.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.81
OTHER INFORMATION: EST HUMAN HIT: BE734284.1, EVALUE 0.00e+00
OTHER INFORMATION: SNISSPROT HIT: P10269, EVALUE 4.00e-26
OTHER INFORMATION: NI HIT: AF208161.1, EVALUE 0.00e+00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 322574, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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                   RESULT 26
US-10-029-386-4312/c
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Score 353; DB 17;
Pred. No. 1.3e-97;
2; Mismatches 30;
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR PRILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
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PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASESEQ for Windows Version 4.0
SEG ID NO 322574
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| DCATION: (1)...(551)
| OTHER INFORMATION: n = A,T,C
| US-10-027-632-322574
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Best Local Similarity 92.0%;
Matches 412; Conservative
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Delymorphisms in the Human Genome FILE REFERENCE: 108827.128 CURRENT APPLICATION NUMBER: US/10/027,632
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Pred. No. 1.3e-97;
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   PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/199,676
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PLILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PLILING DATE: 1999-11-23
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
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Publication No. US20030204075A9
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               = A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 92.0%;
Matches 412; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(551)
; OTHER INFORMATION: n
US-10-027-632-322575
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US-10-027-632-322574
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                                                                                                                                                           GCACCCCTCCATGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 120
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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30; Indels
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APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REPERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US/017,161
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1393
LENGTH: 822900
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OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (85854)...(85953)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (17785). (17884)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (4966)..(4966)
OTHER INFORMATION: a, t, c, g, unknown
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(534176)..(534210)
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LOCATION: (67605)..(67704)
OTHER INFORMATION: a, t, c,
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(273663)..(273702)
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(482589)..(482596)
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NAME/KEY: modified_base
LOCATION: (61159). (61258)
OTHER INFORMATION: a, t, c,
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(140545)..(140693)
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(261786)..(261845)
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LOCATION: (4848)..(4947)
OTHER INFORMATION: a, t, c,
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ORGANISM: Homo sapiens
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LOCATION:
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                           CURRENT AFPLICATION NUMBER: US/10/02/,022, 022, 04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR FILING DATE: 1990-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: PSESSEE OF WINDOWS VETSION 4.0

SOFTWARE: 551
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             CURRENT APPLICATION NUMBER: US/10/027,632
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Publication No. US20030235833A1
GENERAL INPORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAM, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(551)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-322575
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US-10-292-798-1393/c
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FEATURE:
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FEATURE:
NAME/KEY: modified base
LOCATION: (724960)...(725059)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (409961)...(410060)
OTHER INFORMATION: a, t, c, g, unknown or other
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FORTION: (370285)...(370287)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (370289) .. (370291)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (367588) ...(367588)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (367595)...(367595)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (367613) ... (367614)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (367993) ... (367993)
OTHER INFORMATION: a, t, c, g, unknown or other
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INFORMATION: a, t, c, g, unknown or other
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INFORMATION: a, t, c, g, unknown or other
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LOCATION: (370281)..(370282)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (367573)..(367573)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (726106)..(726205)
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LOCATION: (744360)...(744459)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified base
LOCATION: (734441)...(734441)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                             LOCATION: (728849)...(728948)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified base
LOCATION: (730296)...(730395)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (731863) ...(731962)
DIHER INFORMATION: a, t, c, g, unknown
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LOCATION: (734124)..(734223)
OTHER INFORMATION: a, t, c, g,
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LOCATION: (738576)..(738675)
OTHER INFORMATION: a, t, c, g,
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LOCATION: (740924)...(741023)
OTHER INFORMATION: a, t, c, g,
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LOCATION: (735752)..(735851)
OTHER INFORMATION: a, t, c, g,
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                                                     FEATURE:
NAME/KEY: modified base
LOCATION: (727470)...(727569)
OTHER INFORMATION: a, t, c,
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LOCATION: (754323)...(754422)
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Best Local Similarity 68.55
Matches 486; Conservative
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NAME/KEY: modified base
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NAME/KEY: modified_base
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APPLICANT: FLANCE
BESEME, FRELL.
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TITLE OF INVENTION: VITEM MATERIAL AND NUCLEOTIDE FRAGMENTS
THERAPEUTIC PURPOSES
THERAPEUTIC PURPOSES
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                                                                                                                     Score 302; DB 8;
Pred. No. 1.1e-81;
0; Mismatches 25
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FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 08/979,847
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 108, Application US/10114104 Publication No. US20030198647A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRI
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
                                                                                                                         20.4%;
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ZIP: 22320
COMPUTER READABLE FORM:
                                                                                                                       Query Match
Best Local Similarity 92.7
Matches 317; Conservative
TYPE: nucleic acid
STRANDEDNESS: single
      TYPE: nucleic acid

TYPE: nucleic acid

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-979-847-108
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APPLICANT: BESEME, FREDERIC
APPLICANT: BESEME, FREDERIC
APPLICANT: BESIME, FREDERIC
APPLICANT: BADIN, FREDERIC
APPLICANT: CAMUSIAN-PRADEL, FLORENCE
APPLICANT: MANDRAND, BERNARD
APPLICANT: MANDRAND, BERNARD
APPLICANT: TUKE, PHILIP
APPLICANT: TUKE, PHILIP
APPLICANT: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
TITLE OF INVENTION: THERAPEUTIC PURPOSES
TITLE OF INVENTION: THERAPEUTIC PURPOSES
CORRESPONDENCE ADDRESS: 210
CORRESPONDENCE ADDRESS:
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                                       56723 IGGAATGAATTGCCAACTCCCTAGTGACCCTACAAAGCCAGCTTAATTCTTAGCTGCAG
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    TGGAACAGGTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAG
                                                                                      1133 TAGTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAAACGCCCAAAAGAGGGGGAACCTGTT
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979,847

FILING DATE: 26-NOV-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 39046A

TELECOMMUNICATION INFORMATION:

TELECHONE: 703-835-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 108, Application US/08979847
Publication No. US20030039664A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
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US-08-979-847-108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: MAP TO AL022067.1

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.95

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BLACEMYA, SIGNAL = 7.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PTLING DATE: 2001-01-30
PRIOR PTLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
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PRIOR PILING DATE: 2001-01-39
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ORGANISM: Homo sapiens
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                     NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 108:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-114-104-108
                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1329 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.77
Matches 317; Conservative
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Best Local Similarity 88.7
Matches 260; Conservative
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NAME/KEY: misc_feature
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US-10-027-632-86541/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 GCCTATITAATACCACCCTCACTGGGCTCCATGAAGCCTCAG-AGAAACCCTACTAACT 387
                                                                                                                                                                                                                             APPLICANT: Wang, Joavid G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERBUCE: 108627.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR FILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-04-20
FRIOR PRICATION NUMBER: US 60/198,676
FRIOR FILING DATE: 2000-04-20
FRIOR FILING DATE: 2000-04-20
FRIOR PLICATION NUMBER: US 60/193,483
FRIOR FILING DATE: 2000-02-24
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   377 AAAAACAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACATAGCACCCCTAGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497 GCCTATTTAATACCACCCTCACTCGGCTCCATGAGGTCTCAGCCCCAAAACCCTACTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Sequence 316412, Application US/20030204075A9
Publication No. US20030204075A9
GENERAL INFORMATION
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.5%; Score 229.8; DB 13; Best Local Similarity 88.7%; Pred. No. 1.3e-59; Matches 260; Conservative 0; Mismatches 32;
                                                                                                                                                          Sequence 316412, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
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) LOCATION: (1)...(625)

) OTHER INFORMATION: n = A,T,C or G

US-10-027-632-316412
421 ACCCCA 426
                                                                                                          RESULT 35
US-10-027-632-316412/c
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US-10-027-632-316412/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 316412
LENGTH: 625
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Polymorphisms in the Human Genome
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ches 32;
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                TILLE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/02/02/02/03/05
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 1999-01-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-01-23
PRIOR FILING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 325720
SECTWARRE PRESERVE FALSERY FOR WINDOWS VETSION 4.00
SEQ ID NO 316412
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OTHER INFORMATION: n = A,T,C or G
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Gaps

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US-09-664-761-7501, Application US/09864761

Jeatent No. US202004873A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
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APPLICANT: Hanzel, David K.
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APPLICANTON: HANN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITITLE OF INVENTION: HANN GENOME-DERIVED SINGLE EXCON NUCLEIC ACID PROBES USE OF 1200-02-04
FILE REFERENCE: Acomica-X-1
CURRENT FILING DATE: 2001-05-13
FRIOR PAPLICATION NUMBER: US 60/180,312
FRIOR APPLICATION NUMBER: US 60/180,3366
FRIOR APPLICATION NUMBER: US 60/180,3366
FRIOR APPLICATION NUMBER: US 60/180,100666
FRIOR PAPLICATION NUMBER: US PCT/US01/00666
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
FRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                               40; Indels
                                                                                                                                                                                                                        Score 229.6; DB 1
Pred. No. 1.5e-59;
0; Mismatches 40
                                                                                   NAME/KEY: misc_feature
| LOCATION: (1) ... (619)
| CTHER INFORMATION: n = A,T,C or G
US-10-027-632-86541
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86.3%;
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Matches 253; Conservative
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Best Local Similarity
                                     ORGANISM: Human
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GENERAL INFORMATION:
GENERAL INFORMATION:
JULIE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Oblymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/006
FRIOR APPLICATION NUMBER: US 60/218,006
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-07-12
FRIOR PELING DATE: 2000-04-20
FRIOR APPLICATION NUMBER: US 60/199,676
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/195,218
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR PILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR PILING DATE: 1999-11-23
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR FILING DATE: 1999-108-08-09
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-12-33
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PaetSEQ for Windows Version 4.0
SENGTH: 619
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SOFTWARE: FactSEQ for Windows Version 4.0
SEQ ID NO 86541
LENGTH: 619
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                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(619)
OTHER INFORMATION: n = A,T,C or G
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US-10-027-632-86541/c
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CTHER INFORMATION: MAP TO AP001697.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.91

OTHER INFORMATION: OTHER STATES IN HELA, SIGNAL = 0.91

OTHER INFORMATION: SYRESSED IN HELA, SIGNAL = 0.01

OTHER INFORMATION: SYRESSED IN HELA, SIGNAL = 0.000-102

OTHER INFORMATION: SYRESSED IN HELA, SIGNAL = 0.000-102

OTHER INFORMATION: SYRESSED IN HELA, SYALUE 1.000-108

US-10-029-386-20259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
14.4%; Score 213; DB 16; Length 494;
Best Local Similarity 85.6%; Pred. No. 1.7e-54;
Matches 261; Conservative 0; Mismatches 40; Indels
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Publication No. US20030194704A1
GENERAL INFORMATION:
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GENERAL Hanzel, David K.
APPLICANT:
HANZEL OF INVENTION:
GENERAL APPLICANT:
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Pred. No. 2e-56;
0; Mismatches 21; Indels 0
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HERA, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN HERAT, SIGNAL = 2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BABIN, SIGNAL = 1.9
       PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2000-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR PILICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 7501
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Best Local Similarity 91.7%;
Matches 232; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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Direct Submission

Submitted (20-UIL-2004) Genoscope - Centre National de Sequencage :

Submitted (20-UIL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr |

18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-etrand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers

1. .2500

/ organism="Homo sapiens"
/ AD xref="Laxon:9666"
/ Clone="CSODIO51YM13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CK622175
Eull-length cDNA clone CS0DI051YM13 of Placenta Cot 25-normalized of Homo sapiens (human).
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Pred. No. 0;
0; Mismatches
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/plasmid="pCMVSPORT_6"
 BX430050
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Homo sapiens (human)
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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	Ζ Σ	DOURNAL Unpublished  Unpublished  Unpublished  Unpublished  REMARK Conteact: Feng Liang Email: fliang@lifetech.com URL:  http://fulllength.invitrogen.com/ InVitroGen Corporation 1600  REFERENCE 2 (bases 1 to 2748)  AUTHORS Genoscope.  TITLE  AUTHORS Direct Submission  JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:  - Web : www.genoscope.cns.fr  - Web : www.genoscope	/Organism="Homo sapiens" /mol_type="mixA" /mol_type="mixA" /do_ne=CSODE012V34" /tissue type="Placenta" /plasmid="pCMVSPORT_6" /plasmid="p
61 GCACCCCCTCCATGCTGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA 120  833 GCACCCCCTCCATGCGCTGTATGACCAGTAGCTCCCCTTACCAAGAGTTTCTATGGAGA 892  121 ACGCGGCTTCCTGGAAATATTGATGCCCCATCATATGGAGTTTTCTAAGGGAAACTCC 180	121 AGCACCCCTAGCCCCTACAAGGACTAGTTCTCTCAAAACTACATGAAACCCTCCGTACC	3 1 3 1 3 1 3 1 4 4 4 4 4 4 4 4 4 4 4 4	901 ACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCACAACAAAAGAGTACCCATT 960 1673 ACTGAACAAGATTTATACAATTATGTCATACTCTAAGCCCCGCAACAAAAGAGTACCCATT 1732 961 CTTCCTTTTGTTATACAGTGATAGTGCTAGGCAGCAGCAACAAAAGAGTACCCATT 1732 1733 CTTCCTTTTGTTATAGAGCAGGAGTGCTAGGTGCATAGGTACTGGCAGTTC 1020 1733 CTTCCTTTTGTTATAGAGCAGGAGTGCTAGGTGCATAGGTACTTGGCAGTACT 1792 1021 ACAACCTCTACTACTACTACAACTTAGTAGTGCATAGATGGAGCAGTACT 1792 1793 ACAACCTCTACTAGTTATAGAACTTACTACAGAACTAAATGGGGACATGGAACG 1080 1793 ACAACCTCTACTAGTTACTACAAACTATACTCCAAGAACTAATGGGGAACTAGAACG 1140 1793 ACAACCTCTACTAGTTACTACAAAACTATACTCCCTAGCAGCAGTAGTCCTT 1140 1853 GTCGCCGACTCCTTGCAAGATCAACTAAACTCCCTAGCAGTAGTCCTT 1140 1141 CAAAATGGAAGCTTTAGAACTTGCTAACGCCAAAAGAGGGGAACCTGTTTATTTA

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
BP 191 9100 GENYY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
BP 191 9100 GENYY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
181 strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library into normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
                                                                                                                                                                                  1381 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1440
                                                                                                                                                                                                                                                                                                                             CR625046 2748 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI044YK06 of Placenta Cot 25-normalized of Homo sapiens (human).
                                                                                                                                 CTCAGCCAATGGATGCCCTGGGTTCTCCCTTTTAGGACCTCTAGCAGCTCTAATATTG 1380
CAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTTATTTTA 1971
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1 (Dases 1 to 2748)
1 i.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
                          1 AIGGCCCTCCCTATCATACTITICICITIACIGITCTCTTACCCCCTTTCGCTCTCACT
                                                                            1261 ATTCGAGATCGAATACAATGTAGAGCAGGAGCTTCAAAACACCGAACGCTGGGGCCTC
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                                                                                                                                                Gaps
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/organism="Homo sapiens"
/mol_type="mRNN"
/db_xref="taxon:9606"
/clone="CSOD1044YR06"
/tissue_type="placenta Cot 25/plasmid="pCMVSPORT_6"
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Oy 1201 GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAGTTAAAGAA 1260  Db 1983 GGGAAGAATGCTTATTATGTTAATCAATCCGGAATCGTCACTGAGAAGTTAAAGAA 2042  Oy 1261 ATTCGAGATCGATTATATGTTAATCAATCGAGACGCTCGAGAACGCTGGGGCCTC 1320  Db 2043 ATTCGAGATCGAATACAACGTAGAGGAGGAGCTTCGAAACACGGACGCTGGGGCCTC 1320  Oy 1321 CTCAGCCAATGGATGCCCTGGTTCTCTTAGGACCTCTAGGACCTCTAGGGCCTC 2102  Oy 1381 TTACTCCTTTTGGATCCTTTAATCTTTAGGACCTCTAGGAGCTTATAATTG 2162  Oy 1381 TTACTCCTTTTGGACCCTGTATCTTTAGGACCTCTTAGGAGCTTTTAATTTG 2162  Oy 1381 TTACTCCTTTTGGACCCTGTATCTTTAAGATTTGTCTTTCCAGAATT 1440  Db 2163 CTCAGCCCAATGGATGCTTTAACCTCCTTTTTAAGTTTGTCTTTCCAGAATT 1202  Oy 1381 TTACTCCTTTTGGACCCTGTATCTTTAAGATTTGTCTTTCCAGAATT 1440  Db 2123 GAAGCTGTAAAAGTTACAATGGACCCTTGTTAACTTTGTCTTTCCAGAATT 1410	RESULT 5 CR617248 CR617248 CR617248 LOCUS DEFINITION full-length cDNA clone CS0D1022YJ18 of Placenta Cot 25-normalized DEFINITION of Homo sapiens (human). CR617248.1 GI:50498055 KEYWORDS HCC; CNSIT_CDNA. SOURCE HOMO sapiens (human) ORGANISM HCC; CNSIT_CDNA. MARMAlla; Butheria; Primates; Catarrhin; Hominidae; Homo. REFERENCE AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D. TITLE FULL-length cDNA libraries and normalization AUTHORS LI, W.B., Gruber, C., Jessee, J. and Polayes, D. TITLE Full-length cDNA libraries and normalization		ch 1. Similari 389; Cons 1. ATGGCCC         77 ATGGCCC 61 GCACCCC 61 GCACCCC
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Oy 1201 GGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGT	Db 1977 GGGGAAGAATGCTGTTATTATGTTAATCAATCCGGAATCGTCACTGAGAAGT	Oy 1261 ATTCGAGATCGAATACAATGTAGAGCGAGCGTCAAAACCCGAACGCTG	Oy 1321 CTCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCT	Oy 1381 TIACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTC  Db 2157 CTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTTTG	Qy 1441 GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481 		z o z	KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut	REFERENCE 1 (Dasse 1 to 935) AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D. TITLE Full-length cDNA libraries and normalization	JOURNAL Unpublished (2001)  COMMENT Contact: Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRA	Email: secret@genoscope.cns.fr, Web : www.genoscope.cns lst strand cDNA was primed with a NotI-oligo(dT) primer end enriched, double-strand cDNA was digested with Not into the Not I and EcoR V sites of the pCMVSPORT 6 vect.	was normalized. Library was constructed by Life Technol division of Invitrogen. This sequence belongs to sequen 4215.r. For more information about this cluster, see	http://www.genoscope.cns.tr/cdna?s=CS0BAI022ZAI0_CS0208 FEATURES Location/Qualifiers source 1935	/organism="Homo sapiens" /mol_type="mkNa" /db_xref="taxon:9606" /clone="CSODI051YM13"	/tissue_type="PLACENTA_COT_25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA_COT_25-NORMA- /note="list strand cDNA was primed with a NotI primer. Five prime end enriched, double-strand	digested with Not I and cloned into the Not I sites of the pCMVSPORT 6 vector. Library was n	Query Match 56.7%; Score 839; DB 5; Length 935; Best Local Similarity 94.2%; Pred. No. 5.8e-237; Matches 880; Conservative 0; Mismatches 53; Indels 1;	9y 225 TGCCACTCTTTGCATGCAAATACTCATTATTGGACAGGAAAATGATTA 	
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Contact: Genoscope
Genoscope - Centrar National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequenceSope.cns.fr, Web: www.genoscope.cns.fr
Enail: sequenceSope.cns.fr, Web: www.genoscope.cns.fr
lst strand CDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/organism="Homo sapiens"
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BX347952 GI:30375235
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/ Organism="Homo sapiens"

/ Organism="Homo sapiens"

/ Mo _ Lype="mRNA"

/ Clone="CSODIO51YM13"

/ Clone= TSODIO51YM13"

/ Clone= Type="FLACENTA COT 25-NORMALIZED"

/ Clone="Ist strand CDNA was primed with a NotI-oligo(dT)

/ Note="ist strand CDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was primed with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized."
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
1st estrand cDNA was primed with a Not1-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAF027ZB05_AF02531_1&C=4215.r
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COT 25-NORMALIZED HOMO sapiens CDNA
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Homo sapiens
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 931)
Liv.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
                                                                                      | GGTGACAT - GGAACAGGTCACTGACTCCCTGG - TCACCTTGCAGATCAACTTAACTCCC
                    GCCTATCATTGTTTGAATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCC
                                 CCTATGACCATCTACACTGAACAAGATTTATACAATCATGTCGTACCTAAGCCCCACAAC
                                                                                                                                         GGCATTGGCGGTATCACACCTCTACTCACTTCTACTACANACTATCTCAAGAACTAAAT
                                                                                                                                                                                                                                             840 GGGGACATGGGAACGGTTCGCCGACTTCCTGGTTCACCTTGCAAGATCAACTTAACCTCC
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BX389656 Homo sapiens PLACENTA COT 25-NORM
clone CSODIO51YM13 5-PRIME, mRNA sequence.
BX389656.
BX389656.1 GI:30462930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 50.8%; Score 752.2; DB 5; Best Local Similarity 92.3%; Pred. No. 3.3e-211; Matches 856; Conservative 0; Mismatches 65;
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AUTHORS
TITLE
JOURNAL
COMMENT
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BX389656
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us-09-319-156b-9.rst

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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotL-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
double-strand cDNA was digested with Not I and cloned
the Not I and BCORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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1 (bases 1 to 903)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                               TAGTGCCCCCTATGACCATCTACACTGAACAAGATTTATACAATCATGTCGTACCTAAGC 937
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                                                                                                                                                                                                                 AAATAAATGGTGACATGGAACAGGTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTA
On May 13, 2003 this sequence version replaced gi:30648825.
Contact: Genoscope
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For more information about this cluster, see
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DE013XI20"
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime-
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCRWSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 872)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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Pred. No. 9.7e-210;
0; Mismatches 64;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DI051YM13"
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milarity 92.3%; E
Conservative 0;
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invirogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="PLACENTA"
/close lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and BCORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                               This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAA008ZE02_CS00686_1&c=4215.r
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                                                                   Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/clone="CS0DE012YJ24"
                 Chordata;
Primates;
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               Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 883)
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BX388766.2 GI:46877917
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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        TTAATACCCCCTCACTCGCTCCATGAGGTCTC-AGCCCAAAACCCTACTAACTGTTGG
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequeségenoscope.cns.fr. Web: www.oscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSFORT & vector Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAD009ZB06_AD00811_1&c=4215.r
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/tissue type="PEACENYA COT 25-NORMALIZED"
/tissue type="PEACENYA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENYA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand CDNA, was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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11 (Dases 1 to 877)
11 (M.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
                                                                                                          AATGCATCAGGGTGGGTAACTCCTTCCACACAATAGTCTGCCTACCCTCA-GAATATTT
                                                                                                                                                                                                                                                                                TITGICIGIGGIACCICAGCCIAICAITGITIGAAIGGCIC-TICAGAAICIAIGICTI
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                                                GCACAGAAATAAACACCACTTCCGTTTTAGTAGGACCTCTTGTTTCCAATCTGGAAATAA
                                                                                                                                                      CCCATACCTCAAACCTCACCTGTGTAAAATTTAGCAATACTATAGACACAACCAGCTCCC
CCACCCTCACGGGCTCCATGAGGTCTCGGCCCCAAAACCCTACTAACTGTTGGATATGCC
                              TCCCCCTGCACTTCAGGCCATACATTCCAATCCCTGTTCCTGAACAATGGAACAACTTCA
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Pred. No. 3.7e-204;
0; Mismatches 55;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 93.2
Matches 803; Conservative
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/tissue type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
/inche="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     division of Invitrogen.
This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAA0082E02_CS00686_2&c=4215.r
                                                                                                                                                                                                                   1283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAMUS/34 10mO Sapiens PLACENTA HOMO Sapiens CDNA clone CSODE012YJ24
5-FRIME, MENA Sequence.
                                                                                                                                                                                                                                                                                   116
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 921)
   GCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTTCAAAATGGAAGAGCTTTAAGACTT
                                                                                                                                                                                                                                                                                175 TAATCAATCCGGAATCGTCACTGAGAAGTTAAAGAAATTCGAGATCGAATACAACGTAG
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                                                                                                                                                                                                                          TAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAG
                                                                                                                                                                                                                                                                                                                                             1284 AGCAGAGGAGCTTCAAAACACCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                       115 AgcadadadactricaAAACACricaGCCCricaGCCTCAGCCAATGGATGCCCTGGAT
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                                                                                                      GCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTTAGGAGAAGAACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 709.8; DB 5;
Pred. No. 1.2e-198;
0; Mismatches 98;
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/db_xref="taxon:9606"
/clone="CS0DE012YJ24"
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db xrefe="taxon:9606"
/clone="CSODIO44YKN6"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAU012ZB04_U01082_1&c=4215.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                division of Invitrogen. This sequence belongs to sequence cluster
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequed@genoscope.cns.fr, Web : www.genoscope.cns.fr
Enail: sequed@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a Noti-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSULGZYEZ1"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a Not1-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                       For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAU010ZB08_U0922_1&c=7108.r. Location/Qualifiers
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Pull-length cDNA libraries and normalization Unpublished (2001)
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Pred. No. 1.8e-197;
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ilarity 92.7%;
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BX347111 GI:30375145
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 844)
                                                                                                                                       CCCATACCAGTATGTCTGATGGGGGTGGAATTCAAGGTCAGGCAAGAGAAAAACAAGTAA
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                                                      CATCATATAGGAGTTTATCTAAGGGAAACTCCACCTTCACTGCCCACACCCATATGCCCC
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On May 8, 2003 this sequence version replaced gi:30447710.
Contact: Genoscope
Contact: Genoscope
Cenoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCWNSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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BX368078 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI051YM13 3-PRIME, mRNA sequence.
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CTCTTTGCATGCALATACTCATTATTGGACAGGAAAAATGATTAATCCTAGTTGTC 187
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1. (bases 1 to 846)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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                                                                                                                                                                                                                                                     308 cccedegracarcercraecceracaaaccacracaaaccaccacacaaaccacaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       668 CTCCCACACAAIAGTCTGCCTACCTCAGGAAIAITTTTTGTCTGTGTTACCTCAACCT
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                                             CTGGAGGACTTGGAGCCACTGTCGTTGGACTTCACCCATACCAGTATGTCTGATG
                                                                                                                                                                                                                                                                                            CCCTCCGTACCCCATACTCGCCTGGTGAGCCTATTTAATACCACCCTCACTCGGCTCCATG
                                                                                                                                                                                                                                                                                                                                     368 cccrcccraccaracrcccrrccracrarccrarrinarraccaccrcacrccarc
                                                                                                                                                                                                                                                                                                                                                                              AGGICICAGCCCAAAACCCTACTAACTGTTGGATGTGCCTCCCCCTGCACTTCAGGCCAT
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TITLE
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                            1219
                                                                                                                                                                            1279
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BX367907 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI051YM13 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAT022ZG01_T02023_1&c=4215.r. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
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/flone="Ib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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1 (bases 1 to 838)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                    CCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAG
            CCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAG
                                                                                            1160 ACTIGCTAACCGCCAAAAGAGGGGGAACCIGTTTATTTTAGGAGAAGAACGCTGTTATT
                                                                                                                                 1220 ATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAAT
                                                                                                                                                                                                                117 ATGTTAATCAATCCGGAATCGTCACTGAGAAGTTAAAGAAATTCGAGATCGAATACAAC
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                                                                                                                                                                                                                                                           GTAGAGCAGAGGAGCTTCAAAACACCGAACGCTGGGGGCCTCC 1321
                                                                                                                                                                                                                                                                                     GTAGAGCAGAGCAGCTTCGAAACACTGGACCTGGGCCGCCC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.5%; Score 703.2; DB 5;
llarity 93.8%; Pred. No. 1.1e-196;
Conservative 0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX367907
BX367907.1 GI:30459586
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Best Local Simil
Matches 754; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
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AUTHORS
TITLE
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COMMENT
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BX367907
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On May 2003 this sequence version replaced gi:30462931.
Contact: Genoscope Centre National de Sequencage
Genoscope - Centre National de Sequencage
Z rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAF027ZB05_AF02531_2&c=4215.r
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                                                                                                                                                                                                              EST 29-APR-2004
                                                                                                                                                                                                          BX189657
BX389657 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI051XM13 5-PRIME, mRNA sequence.
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/close_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
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1243 ACTGAGAAAGTTAAAGAAATTCGAGATGCAATACAATGTAGAGCGGAGGGGCTTCAAAAC
                   66 ACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAACGT-GAGCAGAGGAGCTTCGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (bases 1 to 995)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Til-length cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 1.4e-194;
0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                              GI:46875146
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86.8%;
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Best Local Si
Matches 826,
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AUTHORS
TITLE
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COMMENT
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BX389657
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                             For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOAU012ZD05_U01092_1&c=4215.r. Location/Qualifiers
                                                                                                                           /mol_type="mRNA"
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/note="list strand cDNA was primed with a NotI-oligo(dT)
/note="list strand cDNA was primed with a NotI oligo (dT)
/note="list strand cDNA was primed with a NotI oligo (dT)
/note="list strand cDNA was digested with Not I and cloned into the Not I and EcoR values of the pCMVSPORT 6 vector. Library was normalized.
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Pred. No. 2.5e-195;
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/organism="Homo sapiens"
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AGCAATACTATAGACACAACCAGCTCCCAATGCATCAGGTGGGTAACACCTCCCACACGA 780
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Corganism="Homo sapiens"

/mol_type="mRMA"

/db xrefp="mRMA"

/clone="CSOD1044YX06"

/clone="Lype="PLACENTA COT 25-NORMALIZED"

/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="lst strand cDNA was primed with a NotI-oligo(dT)

/note="lst prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                            For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAA016ZH06_CS01489_1&c=4215.
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division of Invitrogen. This sequence belongs
                                                                                                                                                                                                                                                                                                                      Score 695; DB 5;
Pred. No. 3e-194;
0; Mismatches 57;
                                                                               Location/Qualifiers
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ilarity 92.7%;
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Best Local Similarity
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies,
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1. (bases 1 to 924)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                          720 TGCTAGGTGCACTAGATCCTGCCATTGGTGGAATAACATCCTTTATTCATTTCTACTACA
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                                                                     GCCTCCCCCTGCACTTCAGGCCATACATTTCAATCCCTGTTCCTGAACAATGGAACAACT
                                                                                                      GCCTCCCCCTGAACTTCAGGCCATATGTTTCAATCCCTGTACCTGAACAATGGAACAACT
                                                                                                                                        TCAGCACAGAAATAAACACCACTTCCGTTTTAGTAGGACCTCTTGTTTCCAATCTGGAAA
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Vencer, J.C.

Vencer, J.C.

Use a random human BAC End Sequence Database for Sequence-Ready
Map Building
Lupublished (1998)
Other_GSSs: CITB1-E1-2506C15.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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AQ261133.1 GI:3787657
                                                                                                                                                                                     1045 AAACTATCTCAAGAAATAAATGGTGACATGGAACAGGTCACTGACTCCCTGGTCACCTTG 1104
                                                                                                                                                                                                                                                           GTGCTAGGCAGACTAGGTACTGGCATTTGGCAGTATCACAACCTCTACTCAGTTCTACTAC 1044
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                                                                                                                                                                                                                                                                                                                                                                           662
                                                                                                                                 363 GTCATATCTAAGCCCCGCAACAAAAGAGTACCCATTCTTCCTTTGTTATAGGAGCAGGA 422
303 ITCCTCTCTTATAGTGCCCCCTATGACCATCTACACTGACAAGATTTATACAGTTAT 362
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/coll type="sperm"
/clone lib="CITB1-B1"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
Calrech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                     603 CTAACCGCTGAAAGANGGGGAACCTGTTTAATTTTAGGGAAGAATGCTGTTATANGTT
                                        GTCGTACCTAAGCCCCCACAAAAGAGTACCCATTCTTCCTTTTGTTATCAGAGCAGGA
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/db_xref="taxon:9606"
/clone="2506C15"
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         831 AGCCATACTACATACACAAATTCCCATGCATCAAGGTGGTAACTCCTCCCACACA 889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hti.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 723)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCAGCACAGAAATAAACACCACTTCCGTTTTAGTAGGACCTCTTGTTTCCAATCTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.7%; Score 647; DB 1; I 94.6%; Pred. No. 4.9e-180; iive 0; Mismatches 38;
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                                                  781 ATAGICIGCCIACCCICAGGAATATITIT 809
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BX409328 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE013YI20 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

Location/Qualifiers
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                                                                                                                                                                                                                                           Score 628.6; DB 1;
Pred. No. 1.4e-174;
0; Mismatches 37;
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                                                                                1. .702
/organism="Homo sapiens"
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/db xref="taxon:9606"
/clone="PLACE1007839"
/clone lib="PLACE1"
/clone lib="PLACE1"
/note="Vector: pME18SFL3"
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llarity 94.6%;
Conservative 0
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Matches 660;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 702)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamofo,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                  181 TIGGAIGIGCTCCCCCTGCACTICAGGCCAIACATITCAAICCCTGTTCCTGAACAAIG
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                       Gaps
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                                                   AAAACAAGTAAAGGAAGCAATCTCCCAACTGACCCGGGGACATAGCACCC
                     Indels
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HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laborantory
Halix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-396
Email: genomics@hri.co.jp
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     7.8e-175;
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      Pred. No. 7.8e
0; Mismatches
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AU138097.1 GI:10999618
      99.84;
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      Local Similarity 99.8
nes 630; Conservative
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BE734284 11H_MGC_21 Homo sapiens CDNA clone IMAGE:3840572 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM530 row: m column: 21 High quality sequence stop: 712.
                                                                                                                                                                                                                                                CAAAACCCTACTAACTGTTGGATGTGCCTCCCCTGCACTTCAGGCCATACATTCAATC
                                                                                                                                                                   ATAGICTGCCTACCCTCAGGAATATTTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CCTGTTCCTGAACAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTA
                                                                                                                                                                                                                                                                                                         GGACCTCTTGTTTCCAATCTGGAAATAACCCATACCTCAAACCTCTGTGTAAAATTT
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/organism="Homo sapiens"
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/ organism="Momo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="CSODE013YI20"
/tissue type="PLACENTA"
/clone lib="Homo aspiens PLACENTA"
/clone lib="Homo aspiens PLACENTA"
/clone lib="weetor: pCMVSPORT 6; lst strand cDNA was primed
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
/with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and BcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-lollgo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAE012ZF02_AE01071_1&c=4215.r
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                                                                                                          Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (2002) 1 (2002)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length CDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30652931.
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Pred. No. 4e-173;
0; Mismatches 120; Indels
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                               GI:46932867
                                                                                                                                                                                                                                                                                                                                                                                                                    division of Invitrogen.
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ilarity 85.5%;
Conservative
                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                     Contact: Genoscope
                                                                                            Homo sapiens
            BX409328
BX409328.2
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Best Local Similarity
Matches 748; Conserv
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                                                                                          ORGANISM
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COMMENT
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KEYWORDS
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On May 15, 2003 this sequence version replaced gi:30776872.
Contact: Genoscope Genoscope Centre National de Sequencage Genoscope - Centre National de Sequencage Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr lst strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and Converted was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                /tissue type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
duth a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                            This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAB002ZD11_CS00181_1&c=4215.r
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Pred. No. 2.7e-160;
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                                                                                                                                                                                                                                                                   1. .658
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE012YJ24"
                                                                                                                                                                                                                                                 Location/Qualifiers
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93.6%;
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Homo sapiens cDNA clone CSODE012YJ24
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                    TGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTACAC
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                                                                                                                                                                                                                AGTCTGCCTACCCTCAGGAATATTTTTGTCTGTGGTACCTCAGCCTATCATTGTTTGAA
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                                                                                                           4,
                                                                         714;
   ZAP-cDNA 8
RT (Life 7
                                                                         Length
                                                                                                          Indels
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Eukaryota, Metazoa, Chordata, Craniata, Verte
Mammalia, Butheria, Primates, Catarrhini, Hon
1 (bases 1 to 658)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
Unpublished (2001)
                                                                     Score 609.8; DB 2;
Pred. No. 5.3e-169;
0; Mismatches 37;
   of California, Berkeley) using (Stratagene) and Superscript II
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BX430050
BX430050.2 GI:47003301
                                                                     41.2%;
llarity 94.3%;
Conservative
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Homo sapiens
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                                                                     Query Match
Best Local Simi]
Matches 676; (
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Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Cenoscope - Centre National de Sequencage
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoNY sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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/tissue type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/clone lib="Wector: PCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAB002ZG11_CS00184_1&c=4215.r
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Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                              421 ATCTCTCAAAACTACATGAAACCCTCCGNACCCATACTCGCCTGGNAAGTCTATTNAATA
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                                                       301 CCCAAACTGGTATGTCTGATGGGGGTGGAGTTCAAGATCAGGCAAGAGAAAAACATGNAA
                                                                                                                                                                                       449 TICICICADADACTACATGADACCCICCGTACCCATACTCGCCTGGTGAGCCTATTTAATA
                                                                                                                                                                                                                                                                              CCACCCTCACTCGGCTCCATGAGGTCTCAGCCCAAAACCCTACTAACTGTTGGATGTGCC
                                                                                                  AGGAAGCAATCTCCCAACTGACCCGGGGACATAGCACCCCTAGGCGCCTACAAAGGACTAG
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Lii, W.B., Gruber, C., Jessee, J. and Polayes, D. Unjul-length cDNA libraries and normalization Unpublished (2001)
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    .814
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    /db_xref="taxon:9606"

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Homo sapiens
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Genoscope - Centre National de Sequencage
Z rue Gaston Cremieux, CP 5706 - 91057 cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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/clone lib="Homo sapiens PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/ncle="Vector: PCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) prImer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAE011ZH12_AE01057_1&c=4215.r
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Homo sapiens cDNA clone CS0DE012XJ24
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1. (bases 1 to 792)

1. (bases 1 to 792)

Full, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 15, 2003 this sequence version replaced gi:30766967.
GCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAGAC 1161
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Pred. No. 5.7e-153;
0; Mismatches 82;
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/db_xref="taxon:9606"
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                                                                                                                                                    792 bp
BX409304 Homo sapiens PLACENTA
5-PRIME, mRNA sequence.
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
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Pred. No. 2.9e-147;
0; Mismatches 31;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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High quality sequence stop: 519.
Location/Qualifiers
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Conservative 0; Mismatches 105;
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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BX450495 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE013Y120
3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1102 TIGCAAGAICAACTIAACTCCCTAGCAGCAGTAGICCTTCA-AAATCGAAGAGCTTTAGA 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1161 CTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTAGGAGAAGAACGCTGTTATTA 1220
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                                                                                                                                                      1041
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Li (Bases I to 700.
Li W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
Onpublished (2001)
On May 22, 2003 this sequence version replaced gi:31018916.
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This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.nns.fr/cdna?s=CSOAU006ZG02_U0495_1&c=4215.r.
Location/Qualifiers
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                                 181 TATGTCATATCTAAGCCCCGCAACAAAGAGTACCCATTCTTCTTTGTTATAGGAGCA
                                                                                                                                                  982 GGAGTGCTAGGCAGACTAGGTACTGGCATTGGCAGTATCACAACCTCTACTCAGTTCTAC
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922 CATGTCGTACCTAAGCCCCCACAAAAAAGAGTACCCATTCTTCCTTTTGTTATCAGAGCA
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/db_xref="taxon:9606"
/clone="CS0DE013Y120"
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            5'-ATTCTAGAGGCGGGGGGGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1576 row: c column: 23
High quality sequence stop: 624.
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BG572445.1 GI:13580098
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ilarity 90.5%;
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                                               Euteleostomi;
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                                                                                                                                                                                                                                                                                                 Email: www.rzpd.de
RZPD; IMAGP958M21530.
RZPDISIB; I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Reubnerweg 6, D-14059 Berlin, Germany
Tel: +449 30 32639 101
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq print prints requence: TTTCACACAGGAAACAGCTATGAC.
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost.

1 (Dases 1 to 554)
Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E.
Ebert,L., Radelof,U. and Schneider,D.
I.M.A.G.E. cDNA Clone Collection
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 554;
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RZPD Deutsches Ressourcenzentrum fuer Genomforschung
Heubnerweg 6, D-14059 Berlin, Germany
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95.0%; Pred. No. 3.6e-129;
ive 0; Mismatches 26;
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sapiens (human)
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/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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IMAGE:3840572 5', mRNA sequence.
CR735592 GI:51584854
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE
Bmail: seqret@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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COT 25-NORMALIZED Homo sapiens CDNA
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Catarrhini, Hominidae; Homo.
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/tissue type="PLACENTA COT 25-NORMALIZED"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                Gaps
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Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30459619.
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Pred. No. 3.9e-113;
0; Mismatches 114;
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/db_xref="taxon:9606"
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Best Local Similarity 81.8%;
Matches 535, Conservative 0
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Homo sapiens
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Mammalia; Eutheria;
1 (bases 1 to 944)
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr. Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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398 AAATGGGGACATGGAACGGGTCGCCGACTCCCTGGTCACCTTGCAAGATCAACTTAACTC 457
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                         Gaps
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Li (bases 1 to 1071)

Li W. B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30374869.
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Pred. No. 9.2e-120;
; Mismatches 53;
                                                                                                                                                                  GGGAACCTGTTTATTTAGGGAAGAATGCTGTTAT
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/db_xref="taxon:9606"
/clone="CSODI046YA18"
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Homo sapiens
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For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAA015ZF07_CS01399_1&c=4215.r
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BX37769.2 GI:46272079
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                                                                                                                                                                  /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Pred. No. 1.3e-111;
); Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                          1. .890
/organism="Homo sapiens"
                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI022YJ18"
                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      28.1%;
83.7%;
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1 (bases 1 to 890)

2 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

3 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

4 Inpublished (2001)

5 On May 2, 2003 this sequence version replaced gi:30342581.

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1st strand cDNA was primed with a NoII-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NoI I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a

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890 bp mRNA linear EST 08-APR-2004
BX326300 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens cDNA
clone CSODI022YJ18 5-PRIME, mRNA sequence.
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                                                                                             GCACCCCCTCCATGCTGCTGTACAACCAGTAGCTCCCCTTACCAAGAGTTTCTATGAAGA
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On May 8, 2003 this sequence version replaced gi:30439129.
On May 8, 2003 this sequence version replaced gi:30439129.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE
Email: sequenceGenoscope.cns.fr, Web : www.genoscope.cns.fr
Beail: sequenceGonoscope.cns.fr, Web : www.genoscope.cns.fr
lst strand cDNA was primed with a NotI.-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                BX378303 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
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1 (bases 1 to 1058)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Pull-length cDNA libraries and normalization
Unpublished (2001)
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//db xref="taxon:9606"
/clone="CSODIO18YHOTA"
/clone="Issue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone list strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                     clone CSODI018YH07 3-PRIME, mRNA sequence
BX378303
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BX378303.2 GI:46557492
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Homo sapiens
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                                                                                                                                                                                                                                                Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer: Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/mol type="manna" aspron.
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/db_xref="taxon:9606"
/clone="CSOBIOSINMA"
/tissue type="PLACENTA COT 25-NORWALIZED"
/clone Tib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                          On May 2, 2003 this sequence version replaced gi:30337641
Contact: Genoscope
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Catarrhini; Hominidae;
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Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases I to 998)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 2.4e-110;
4; Mismatches 42;
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ilarity 90.5%;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 564)

1. (Dases 1 to 564)

1. Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

1. Full-length cDNA libraries and normalization

1. Unpublished (2001)

1. On May 8, 2003 this sequence version replaced gi:30461045.

1. Contact: Genoscope

2. rue Gaston Cremieux, C. P 576.

2. post Saston Cremieux, C. P 576.

2. rue Gaston Cremieux, C. P 576.

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3. rue Gaston Cremieux, C. P 576.

3. rue Gaston Cremieux, C. P 576.

4. sequence cns.fr

1. st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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316 ATGCAGCGTCCCGGAAATATTGATGCCCCATCGTATAGGAGTCTTTCTAAGGGAACCCCC
                                                                                    ACCTTCACTGCCCACCCATATGCCCCGCAACTGCTATAACTCTGCCACTCTTTGCATG
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2 (contact: Genoscope - Centre National de Sequencage
2 contact: Genoscope - Centre National de Sequencage
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3 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
3 rue Gaston Cremieux de Sequence CDNA was Gigested with Not I and cloned into the Not I and ECGRY sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 4215.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?ecSOMT011ZF02_T0974_1&c-4215.r.
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/dlone="CSODE013Y120"
/tissue type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
with a Not1-oligo(dT) primer. Five prime end enriched,
the Not I and CORV wites of the pCMVSPORT 6 vector.
Library was not normalized."
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4X429316 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE013Y120
5-PRIME, mRNA sequence.
BX420316
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                                                         TCAGCCAATGGATGCCCTGGGTTCTCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTGT 1381
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                                                                                                                                                                                               590 TACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTCCAGAAICG
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                                                                                                          650 readecaardeardecerdearrereceerrerradaacereradeaceraraararree
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                                                                                                                                                                                                                                                                       1442 AAGCIGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1481
                                                                                                                                                                                                                                                                                                                     AAGCTGTAAAACTACAAATGGAGCCCAAGATGCAGTCCAA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 411.4; DB 5;
Pred. No. 4.1e-110;
0; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BX429316.2 GI:47035285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local S
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BX429316
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODE012YJ34"
/fisue_type="PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484 bp mRNA linear EST 03-MAY-2004 sapiens PLACENTA Homo sapiens cDNA clone CSODE012YJ24 sequence.
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Int strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

This sequence belongs to sequence cluster 4215.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE012DE12NP1&c=4215.r.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1420 AAGTITGICITICCAGAATTGAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCACTGAGAAAGTTAAAGAAATTCGAGATCGAATACAATGTAGAGCAGAGGAGCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACACCGAACGCTGGGGCCTCCTCAGCCAATGGATGCCCTGGGTTCTCCCCCTTCTTAGGA
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27.1%; Score 402; DB 5; I
Best Local Similarity 90.0%; Pred. No. 2.6e-107;
Matches 434; Conservative 6; Mismatches 41;
                                                                                                                                                                                                                                             /organism="Homo sapiens"
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BX409035 Homo s
3-PRIME, mRNA s
BX409035
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BX439636 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE012XJ24 3-PRIME, mRNA sequence.
BX439636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTCAAGAAATAAATGGTGACATGGAACAGGTCACTGACTCCCTGGTCACCTTGCAAGAT 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAACTTAACTCCCTAGCAGCAGTAGTCCTTCAAAATCGAAGAGCTTTAGACTTGCTAACC 1170
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Li (Bases I to 1019)
Li, W.B., Gruber, C., Gessee, J. and Polayes, D.
Pull-length cDNA libraries and normalization
Ombublished (2001)
On May 15, 2003 this sequence version replaced gi:30771765.
Contact: Genoscope
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/clone=libt_strand_cDNA_was_primed_with_a_NotI-oligo(dT)
primer. Five prime end enriched, double-strand_cDNA_was
digested with Not_I and cloned into the Not_I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                                                                                              ATTCTTAGTGCCCCCTAT - - GACCATCTACACTGAACAAGATTTATACAATCATGTCGTA
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                  2;
                                                                                                                                                                                               Length 564;
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                                                                                                                                                                                           27.4%; Score 406.4; DB 5;
larity 84.4%; Pred. No. 1.1e-108;
Conservative 0; Mismatches 84;
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BX439636/c
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
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                                                                                                                                                                                                                                                                                                                                                 division of Invitrogen.
This sequence belongs to sequence cluster 4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOBAD005ZE05_AD00422_1&c=4215.r
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                                                               Eukaryotz, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryotz, Metazoa, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 484)
1i, W.B., Gruber, C., Jessee, J. and Polayes, D.
1i, W.B., Gruber, C., Jessee, J. and Polayes, D.
10 (bright cDNA libraries and normalization on May 15, 2003 this sequence version replaced gi:30766926.
Contact: Genoscope
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larity 91.9%; Pred. No. 3.1e-107;
Conservative 0; Mismatches 37;
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   GI:46956493
                                        Homo sapiens (human)
                                                             Homo sapiens
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les 445; Conserv
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Matches
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Sequence Human BAC

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AF52053782 AF52054982 AF52055382 AF52056182 AF52056382 AX329572 HSAC000064

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AF52050782 AF52051182 AF52052382 AF52052782 AF52053182

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AF520540 B

ALIGNMENTS

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AC007566 AF520486 AF520492 AF520500

Homo sapi

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unclassified.

1 (Dases 1 to 1329)
Baccala,G.P., Pradel,F.K., Bedin,F., Sodoyer,M., Ott,C., Mallet,F.,
Baccala,G.P., Pradel,F.K., Bedin,F., Sodoyer,M., Ott,C., Mallet,F.,
Berron,H. and Mandrand,B.
Retroviral nucleic material and nucleotide fragments, in
particular, associated with multiple sclerosis and/or rheumatoid
arthritis, for diagnostic, prophylactic and therapeutic uses
BIO MERIEUX
                                                                                                                                                                                                                                                                                                                   BD136199
Retroviral nucleic material and nucleotide fragments, in particular, associated with multiple sclerosis and/or rheumatoid architis, for diagnostic, prophylactic and therapeutic uses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIREILLE SODOYER, CATHERINE OTT, FRANCOIS MALLET, HERVE PERRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-UTL-1998 JP 1999508255
07-JUL-1997 FR 97/08816
GLAUCIA PARAHNOS BACCALA, FLORENCE KOMURIAN PRADEL, FREDERIC
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Retroviral nucleic material and nucleotide fragments,
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Location/Qualifiers
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C12N15/48,C12Q1/70,C07K14/15,A61K31/70
Strandedness: Single;
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BD136199.1 GI:23231144
JP 2002509437-A/9.
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JP 2002509437-A/9
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                                                                    February 21, 2005, 06:32:54; Search time 5704.48 Seconds (without alignments) 11288.850 Million cell updates/sec
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             GenCore version
Copyright (c) 1993 - 2005
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AF52049782
AF52050382
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PAT 18-SEP-2002

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961 G		1081 TGGGTTTGTCCTAATAGAACTGAACACTGGTCCACGGTTCCATGGTTCTTCCATGACTTATAGACTTGTCGTTGTTCATTCCATGACTTATAGACTTAATAAAACTGAACATGACGGAAGATTCCATTCCATGGACTTAAAAAAAA	1141 CCACGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGTA	TCTGTGAGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTGGGAAGTGG	1261 CCCACTGCATTTTGGTAGGGCCCACCACCATCTTGGGAGCTGTGGGAGCAAGGATCCC 1321 CCACTAACA 1329		AR344389	0	NISM	TITLE Isolated nucleotide sequences associated with multiple sclerosis or rheumatoid arthrities and a process of detecting	FEATURES Location/Qualifiers  FOURCE 1. 1329  /organism="unknown" /m] type="mpth"	ORIGIN  Query Match 99.8%; Score 1326; DB 6; Length 1329;	vative 0; Mismatc	Db 1 TCAAAATCGTTTTGTTTTGTAACCGCCAAAAGAGGGGAACCTGTTTATTTT 60 Qy 61 AGGGAAGAATGCTGTTAATCAATCTGAATCTTGAATTACTGAAAGA 120	Db 61 AGGGAAGATGCTGTTAGTTTTTTTTTTTTTTTTTTTTTT	Db 121 AATTTGAGATGAATATAATGTAGAGCAGAGAGCTTTCAAAACACTGCACCTGGGGCCT 180  Qy 181 CCTCAGCCAATGGATGCCCTGGACTTCTTAGGACCTTAGGAGCTATATT 240	Db 181 CCTCAGCCATGGACCCTCGCCTTCTTAGGACCTCTAGCAGTATATT 240  Qy 241 TIACTCCTTTTGACCCTGTATCTTCAGACTTCTTAGGACCTTCTTCAGAT 300
<pre>gource 11329 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"</pre>	Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OY         1         TCAAAATCGAAGGTTTAGACTTGCTAACCGCCAAAGAGGGGGAACCTGTTTATTTTT 60           Db         1         TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGAACCTGTTTATTTTT 60	Qy 61 AGGGGAAGAATGCTGTAGTATGTTAATCAATCTGGAATGATACTGAGAAAGTTAAAGA 120 	Qy     121 AATTTGAGATCGAATATAATGTAGAGCCAGAGGACCTTCAAAACACTGCACCCTGGGCCT 180       Db     121 AATTTGAGATCGAATATAATGTAGAGCAGAGGACCTTCAAAACACTGCACCCTGGGGCCT 180	QY     181 CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATT 240       DD     181 CCTCAGCCAATGGATGCCCTGGACTCTCCCCCTTCTTAGGACCTCTAGCAGCTATAATATT 240	Qy 241 TTACTCCTCTTTGGACCCTGTATCTTCAACTTCTTGTTAAGTTTGTCTTCCAGAAT 300	OY 301 TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA 360 	Oy 361 AATCTACCGTGGACCCTGGACCGCTGCTAGACTATGCTCTGATGTTAATGACATTGA 420 Db 361 AATCTACCGTGGACCCCTGGACCGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA 420	Qy 421 AGTCACCCCTCCCGAGGAAATCTCAACTGCACACCCCTACTACACTCCAATTCAGTAGG 480	Qy 481 AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA 540	Qy 541 GGGTGGACTGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT 600	OY 601 ANCTGGGAAGGTGACGGCATCCATCTTAAACATGGGGCTTGCAACTTAGCTCGCG 660 	OY 661 ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC 720 	Qy 721 AATCATCTATTGCCTGAGAGCACAGGGAGAGACAGGATTGGGATATAAACTCAGGCA 780 	Oy 781 TTCAAGCCAGCAACAGCAACCCCTTTGGGTCCCTCCCATTGTATGGGAGCTCTGTTTT 840	841	OY 901 CTCAAGCTGAGCTTTTGTTCGCCATCCACCTGCTGTTTGCCACCGTCACAGACCCGCT 960

11 THATCH THE THE THE THE THE THE THE THE THE TH	Db 1321 CCAGTAACA 1329	RESULT 3 AX001030 LOCUS DEFINITION Sequence 12 from Patent WO9902666. ACCESSION AX001030 VERSION AX001030 KEYWORDS AX001030.1 GI:7241266 KEYWORDS AX001030.1 GI:7241266 KEYWORDS AX001030.1 GI:7241266	NISM unidentified unclassified. NCE 1 (bases 1 to 1329) ORS Ott.C. and Bedin.P. AMPERIAL AND MICHEOFITHE PRACMENTS	TITLE RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENIS, IN PARTICULAR ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR DIAGNOSTIC, PROPHYLACTIC AND THERABEUTIC USES JOURNAL PACENT: WO 9902666-A 12 21-JAN-1999;	Ö	/mol_type="unassigned DNA" /db_xref="taxon:32644" ORIGIN	Query Match 99.8%; Score 1326; DB 6; Length 1329; Best Local Similarity 100.0%; Pred. No. 0; Matches 1329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGGGGGGAACCTGTTTATTTT 60 	Oy 61 AGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGA 120 	Qy 121 AATTTGAGATCGAATATAATGTAGAGCAGGACCTTCAAAACACTGCACCCTGGGGCCT 180 	Qy         181         CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATT         240           bb         181         CCTCAGCCAATGGATGCCTTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATT         240	Qy 241 TTTACTCCTCTTTGGACCCTGTATCTTCAACTTGTTAAGTTTGTCTTCCTGGAAT 300	Qy 301 TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA 360 	Qy 361 AATCTACCGTGGACCCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA 420	Qy 421 AGTCACCCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG 480	Qy 481 AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA 540	Qy         541 GGGTGGACTGAGAGACAGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCT 600	Qy 601 ANCTGGGAAGGTGACCGCATCCATTAAACATGGGGCTTGCAACTTAGCTCACACCG 660
TITLE CCTCTTTTTGATCTTCAACTTCAACTTCCTTGTTTAACTTTGTTCTCTTCTCTCTC						,		<del></del>								•		<del>:</del> :
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us-09-319-156b-12.rge

TITLE Direct Submission JOURNAL Submitted (16-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell JOURNAL Submitted (16-NOV-2001) DOE Joint Genome Institute, Walnut Creek, CA 94599, USA COMMENT On Nov 16, 2001 this sequence version replaced gi:15383820. Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov Finishing Completed at Stanford Human Genome Center www.sigc.stanford.edu Quality: Phrap Quality >=40 99.8% of Sequence; Estimated Total Number of Errors is 0.3. FEATURES 1163803   /organism="Homo sapiens"	OUETY Match  Query Match  Query Match  Best Local Similarity 99.3%; Pred. No. 0;  Matches 1320; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  Matches 1320; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  Qy   12   ADGGGAAGAGCTTTAGACTTGCTAACCGCCAAAGAGGGGAACCTGTTTATTTT 17545  Qy   12   AATTGAGATGCTTAGTTGTTAATCATCTGGAATCATTACTGAAAGTTAAAGA 117485  Qy   12   AATTGAGATGCTATAGTAGTAGTAGTGGAAGCTTACTGGAAAGTTAAAGA 117485  Db   117544 AGGGGAAGAATGTTAATGTAGAGGAGGAGCCTTCAAAACCTGGGGGCCT 180  Qy   12   AATTTGAGATGTAATATGTAGAGGAGGACCTTCAAAACCTGCACCCTGGGGCCT 180  Db   117484 AATTTGAGATCAATATAAAGAGAGGACCTTCAAAACATGCACCCTGGGGCCT 117425	181 117424 241 117364 301 117304	
Db   601 ANCTGGGAAGGTGACCGCATCCATTTAAACATGGGGCTTGCAACTTAGCTCACCCCG   660	0   0   0   0   0   0   0   0   0   0	Qy         1141         CCACGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCTTGGTA         1200           Db         1141         CCACGGCTTCTAATAGAGCTATAACACTCACCGCATGCCACAATTCCTTGGTA         1200           Qy         1201         TCTGTGAGGCCAAGAACCCCAAGAACTGCCACCATTTGGGAAGTGG         1260           Db         1201         TCTGTGAGGCCAAGAACCCCAAGAAACTGCAACATTGCAACATTTGGGAAGTGG         1260           Qy         1261         CCCACTGCCATTTGGTAGCGGCCCACCATTTGGGAAGTGG         1260           Qy         1261         CCCACTGCCATTTGGTAGCGGCCCACCATTTGGGAAGCACCATTTGGGAAGTGC         1320           Db         1261         CCCACTGCCATTTGGTAGCGGCCCACCATCTTGGGAAGCTGTGGGAAGAAGATCCC         1320           Qy         1321         CCACTGCCATTTTGGTAGCGGCCCACCACCATTTGGGAAGCTGTGGGAACAAGAATCCC         1320           Qy         1321         CCACTGCCATTTTGGTAGCGGCCCACCACCACCATTTGGGAAGCTGTGGGAACAAGAATCCC         1320           Qy         1321         CCACTGCCATTTTGGTAACA         1329           Db         1321         CCAGTAACA         1329	RESULT 4 AC093531 COUS LOCUS DEFINITION AC093531 ACC093531 ACCOMPAL AC

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join (247. .811,2872. .9669)

hote="putative mRNA transcript 1; gag-pol pseudogene

join (247. .811,7440. .9669)

/product="envelope glycoprotein"

/note=="putative mRNA transcript 2"

join (247. .811,9104. .9669)

/note="putative mRNA transcript 3; no coding region"
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'isolation_source="PBMC of orangutan 1"
                                            /note="isolated by PCR; ERVWE1 locus,
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0; Mismatches 130;
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              /db xref="taxon:9600"
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   116884 AATCATCTATTGCCTGAGAGCACAGGGGAAGGACAAGGATTGGGATATAAACCCAGGCA 116825
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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Submitted (06-MAY-2002) Retrovirology Department, UMR 2142
Submitted (06-MAY-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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                                   TICAAGCCAGCAACAGCAACCCCCTITGGGICCCCTCCCATIGIAIGGGAGCTCTGTTIT
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Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G., Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEl is a bona fide gene: in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet, F., Bouton, O. and Oriol, G.
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                                                                   Direct Submission

Submitted (28-00v-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

ON Nov 28, 2002 this sequence version replaced gi:22758291.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov produced at Stanford Human Genome Center

Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.7.
Direct Submission
Submitted (07-SEP-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 14871)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Pred. No. 0;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                           /chromosome="5"
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milarity 88.9%;
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1 (bases 1 to 148711)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission.
                                                                AGCTGGGAAGGTGACCACCATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACTG
                                                                                                                          ACCAATCAGAGAGCTCACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCC
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DOB Joint Genome Institute and Stanford Human Genome Center.
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FLGFRAAITLLLFROFDCIRTLANFVSSRIBANKLQMSEPRASP
 1 (bases I to 2694)
Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWEl is a bona fide gene involved
in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeritux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
Primates; Catarrhini; Hominidae; Homo
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/mol_type="genomic DNA"
/isolate="individual 132 allele i/db xref="taxon:9606"
/chromosome="7"
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/note="splice acceptor site"
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/note="Caucasian
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Homo sapiens individual 132 allele A, envelope glycoprotein gene,
Complete cds, and 3' long terminal repeat, complete sequence.
AF520478
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dasea; 1 to 2694)

Mallet, F., Boucotte, G., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.

The endogenous retroviral locus ERVWEl is a bona fide gene involve in hominoid placental physiology

Proc. Natl. Acad Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeriaux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
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/mol_type="genomic DNA"
/isolate="individual 22 allele
/db_xref="taxon:9606"
/chromosome="7"
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/note="splice acceptor site"
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/note="Caucasian
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AF520489S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 22 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence. AF520490

AF520489S2 LOCUS DEFINITION AF520490.1 GI:33410948

ACCESSION VERSION KEYWORDS

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AF520505S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 37 allele A, envelope glycoprotein gene,

RESULT 10 AF520505S2 LOCUS DEFINITION

Eukaryofa, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2694)
Mallet, F., Bouton, O., Frudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004) 1482 1542 120 180 181 CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTTAGGACCTCTAGCAGCTATAATATT 240 **AGGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGA** AATTTGAGATCGAATATAATGTAGAGCAGAGGACCTTCAAAACACTGCACCCTGGGGCCT TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTT 1423 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTTATTTT Gaps complete cds, and 3' long terminal repeat, complete sequence. AF520506 AF520506.1 GI:33410980 UMR 2142 - 46 allee Length 2694; 13; Maller, F., Bouton, O. and Oriol, G. Direct Submission.
Submitted (Or-UN-2002) Retrovirology Department, CNRS-bioMerieux, Ecole Normale Superieure de Lyon d'Italie, Lyon 69364 cedex 07, France Location/Qualifiers Indels 78.0%; Score 1036.8; DB 9; larity 90.2%; Pred. No. 9.7e-305; Conservative 0; Mismatches 110; <u>-</u> /cell\_type="PBMC's" /note="endogenous\_virus: HERV-W" RSDVNDIKGTPPEEISAAQPLLRPNSAGSS" 1705. .1720 /mol type="genomic DNA" /molate="individual 37 allele /db xref="taxon:9606" /chromosome="7" /note="splice acceptor site" 1959. .2694 /note="splice acceptor site" 284. .1900 1. .2694 /organism="Homo sapiens" note="syncytin" /map="7q21-q22" /sex="male" (bases 1 to 2694) (human) 43. .57 2 of 2 Homo sapiens Homo sapiens Best Local Similarity Matches 1134; Conserv 121 1543 ે 셤 ò involved

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/translation="MALPYHIFLFTVLLPSFTLTAPPPCRCMTSSSPYQEFLWRMQRPGIIDAPSYRGLSKGTPFTAHTHMPRNCYHSATLCMHANTHYWTGKMINPSCPGGLGV
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HTRLVSLFNTTLTGLHEVSAQNPTNCWICLPLNFRPYVSIPVPBQWNNFSTEINTTSV
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- 46 allee
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The endogenous retroviral locus ERVWEI is a bona fide gene in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004) 14757826
                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 2694)

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Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, ISANS-bioMerieux, Ecole Normale Superieure de Lyon d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/codon tetart=1
/product="envelope glycoprotein"
/protein.id="AAQ17887.1"
/db_xref="GI:33411029"
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TTGLIGSTSERNCFLGEBTLYPROWITTYTTNQCIRWTTPPTQLVCLPSGIFFVCGTSA
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YRCLNGSSESGNCFLGFLYPPWTITTTNGCYTLGAPTCAPAGIFFVCGTSA
TGTGGITTGTQFYXTLSQEINGDMERVADSLYTLQDQLNSLAAVULQNRRALDLLTAE
RGGTCLFLGEECCYYVNQSGITVTEKVKEIRDRIQRRAEELRWTGPWGLLSQWMPWILP
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FLGFRAAIILLLFGFPCIFFRAANTSSRIEAVKLQMEPERNGSKTKIYRRPELDRFPASP
                                                                                                                                                                                                                        Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2694)
Maller,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Maller,F., Lucotte,G., Duret,L. and Mandrand,B.,
The endogenous retroviral locus ERVWEl is a bona fide gene involved
in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                11-FEB-2004
                                                                              AF52048382

Homo sapiens individual 147 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
2610 TCCATAAGGCCAAGAACCCCAGGTCAGAGAACACGAGGCTTGCCACCATCTTGGGAG 2666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1423 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTATTTTT
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                                                                                                                                                                                                                                                                                                                                                                                            Mallet,F., Bouton,O. and Oriol,G.
Direct Submission

Direct Submission

CNRS-bioMerieux, Ecole Normale Superfeure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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/db_xref="taxon:9606"
/chromosome="7"
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/note="splice acceptor site"
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/organism="Homo Bapiens"
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                                                                              CCTCAGCCAATGGATGCCCTGGATCTCCCCCTTCTTAGGACCTCTAGCAGCTATAATATT
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FLGFLAAIILLLFGPCIPPREISAAQPLLRPNSSRIEAVKLQMEPRMQSKTKIYRRPLDRPASP
                                                                                                           2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 148 allele B, envelope glycoprotein gene, AF520488
                                                                                                                                                                                                                                                                                                                                                                                                                         involved
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1 (bases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEl is a bona fide gene involve in hominoid placental physiclogy
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Maller,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeriaux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
          1201 TCTGTGAGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTTGGGAAG
                                2610 TCCATAAGGCCAAGAACCCCAGGTCAGAGAACACGAGGCTTGCCACCATCTTGGGAG
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1959. .2694
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Homo sapiens (human)
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AF520487S2
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                                                                                                                                                                                         TITACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT
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Homo sapiens
Homo sapiens
Bokaryota, Macraca, Chordata, Craniata, Vertebrata; Buteleostomi;
Bokaryota, Materia, Primates; Cararrhini, Hominidae, Homo.

1 (bases 1 to 2694)
Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucchte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWEl is a bona fide gene involved
in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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                                                                                                                                                                                                                                   AF520493S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 24 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
                                2551 CCACAGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGGTTCCATTCCTT-GAA 2609
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                                                                                                                    TCTGTGAGGCCAAGAACCCCCAGGTCAGAANGTGAGGCTTGCCACCATTGGGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department,
CNRS-bioMerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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Pred. No. 3e-304;
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1959. .2694
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90.1%;
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                                      AGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGA
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The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                                                    CCACGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGTA 1200
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Direct Submission

Direct Submission

CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France

Location/Qualifiers
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                                                               Gaps
                                                              13;
                              Length 2694;
                              Score 1035.2; DB 9; Length
Pred. No. 3e-304;
0; Mismatches 111; Indels
                              77.9%;
90.1%;
                              Query Match
Best Local Similarity 90.1
Matches 1133; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2694)
Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
Mallet, F., Bouton, O. and Oriol, G.
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Homo sapiens individual 34 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.

AF520504

AF520504.1 GI:33410976
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                                                                                              TGGGTTTGTCCTAATAGAACTGAACACTGGTCCATGGGTTCCATGGTTCTCTTCCATGAC
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Direct Submission
Submitted (Or-JUN-2002) Retrovirology Department,
CNRS-biomerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/organism="Homo sapiens"
/organism="Homo sapiens"
/isolate="individual 34 allele B'
/db_xref="taxon:9606"
/chromosome="7"
/map="7q21-q22"
/sex="male"
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/note="splice acceptor site"
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Pred. No. 3e-304;
0; Mismatches 111; Indels
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TGIGGITTSTOFYYKLSQELNGDMERVADSLYTLQDQLNSLAAVVLQNRRALDLLTAB
RGGTCLFLGEECCYYVNQSGIVTEKVKEIRDRIQRRAEELRNTGPWGLLSQWMPWILP
FLGPLAAIILLLFGPCIFNLLVNFVSSRIEAVKLQMEPKMQSKTKIYRRPLDRPASP
RSDVNDIKGTPPEEISAAQPLLRPNSAGSS"
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Pred. No. 3e-304;
0; Mismatches 111; Indels
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/note="splice acceptor site"
1959. .2694
                                                                                         77.9%;
90.1%;
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Best Local Similarity 90.1
Matches 1133; Conservative
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/translation="walpyhiflelftyllpsptltapppcrcmtssspygeflwrmgrp
gnidapsyrelskgtptftahthmprncyhsatlcmhanthywtgrminpscpgglgv
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2694)
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Homo sapiens individual 45 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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                           GCTGACTTCCATCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGT
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Direct Submission
Submitted (O7-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 63344 cedex 07, France
Location/Qualifiers
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The endogenous retroviral locus ERVWE1 is a bona fide gene in hominoid placental physiology Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004) 14757826
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/sex="man1e"
/note="endogenous_virus: HERV-W"
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/protein_id="AAQ17577.1"
/db_xref="G1:33410989"
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/organism="Homo sapiens"
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/db xref="taxon:9606"
/chromosome="7"
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/note="splice acceptor
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note="syncytin"
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AF520513S2 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 49 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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Bukaryota.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,

Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.

The endogenous retroviral locus ERVWEI is a bona fide gene involve in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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                                                         CTTGAGCTGAGCTTTCGCTCGCCATCCACCACTGCTGTTTGCCGCCACCGCAGACCGCC
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CTCAAGCTGAGCTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACAGACCCGCT
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Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (O'J-JUN-2002) Retrovirology Department,
CNRS-blowerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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/product="envelope glycoprotein"
/protein_id="AAQ17579.1"
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/mol_type="genomic DNA"
/isolare="individual 49 allele
/db_xref="texon:9606"
/chromosome="7"
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/note="splice acceptor
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/cell_type="PBMC's"
/note="Asian
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/note="syncytin"
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RGGTCLFLGSECCYYNUQSGIYTEKVKEIRDRIQRRAEELRYTGPWGLLSQNMPWILP
FLGPLAAIILLLFGPCIFNLLVNFVSSRIEAVKLQMEPKMQSKTKIYRRPLDRPASP
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Maller, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Maller, F., Bouton, O., Duret, L. and Mandrand, B.
Bonnaud, B., Lucctte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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The endogenous retroviral locus ERVWEI is a bona fide gene involve in hominoid placental physiology Proc. Natl. Acad Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department,
CNRS-bioMeriteux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 63364 cedex 07, France
Location/Qualifiers
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FLGBPLAAIILLLLEGPCTFULVNFVSSRIEAVKLQMEPKMQSKTKIYRRPLDRPASP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Homo sapiens individual 55 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6936 (1911).
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeriatux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 6934 cedex 07, France
Location/Qualifiers
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Pred. No. 3e-304;
0; Mismatches 111; Indels
/sex="female"
/cell_type="PBMC's"
/note="endogenous_virus: HERV-W"
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1705. .1720
//note="splice acceptor site"
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/note="syncytin"
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Matches 1133; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2694)
Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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                                                                                                         ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAAGCAATAGCC
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Direct Submission

Direct Submission

Submitted (07-JUN-2002) Retrovirology Department, UMR 2142

CNRS-bioMeriaux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69346 cedex 07, France

Location/Qualifiers
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Homo sapiens
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Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 2694)
Mallet, F.; Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWEl is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet, F., Bouton, O. and Oriol, G.
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Pred. No. 3e-304;
0; Mismatches 111; Indels
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Best Local Similarity 90.1
Matches 1133; Conservative
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Homo sapiens individual 80 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
Malle, F., Butheria, Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involvin hominoid placental physiology
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                              AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA
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 Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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Pred. No. 3e-304;
0; Mismatches 111; Indels
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1959. .2694
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Arszus3782 2694 bp DNA linear PRI 11-FEB-2004 complete cdB, and 3' long terminal repeat, complete sequence.
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GATCTACCGCAGACCCCTGGACCGGCCTGCTAGCCCACGATCTGATGTAATGACATCAA 1830
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bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Buthoria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2694)
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                                                                                                                               AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTTCCTGTTGAGA
                                                                                                                                                         1891 AAGCAGTTAGAGCGGTCGTCGGCCAACTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
                                                                                                                                                                                                                                                   2011 AGCTGGGAAGGTGACCACATCCACCTTAAACACGGGGCTTGCAACTTAGCTCACACCTG
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  Proc. Nal..

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Rallet,F., Bouton,O. and Oriol,G.

Direct Submission

AL Submitted (07-JUN-2002) Retrovirology Department, UMR CNRS-biomeriteux, Ecole Normale Superieure de Lyon - 4 d'Italie, Lyon 69364 cedex 07, France

Location/Qualifiers

2694
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Pred. No. 3e-304;
0; Mismatches 111; Indels
                                                                                                                                                                                                                                                        /mol_type="genomic_DNA"
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Best Local Similarity 90.1%;
Matches 1133; Conservative (
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Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
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d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
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      Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2694)

Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G., Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.

The endogenous retroviral locus ERVMEl is a bona fide gene invoint hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)

14757826

Mallet,F., Bouton,O. and Oriol,G.

Direct Submission

C. Sibmitted (07-UNN-2002) Retrovirology Department, UMR 2142

CNRS-blowerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
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ive 0; Mismatches 111; Indels
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/isolate="individual 95 allele A"
/db_xref="taxon:9606"
/chromosome="7"
/mop="7021-q22"
/eex="female"
/cell_type="PBMC's"
/note="endogenous_virus: HERV-W"
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                                                                                                   TGAAGCTGTAAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA
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LVGPLVSNLBTTTFTSNLTYTNSQCISWTYPPPOIUVCAPSTEINTTSV
TGLGGTTTSTOFYXKLSQEINGDMSRVADSUSLAAVULQNRARALDLLTAB
RGGTCLFLGEBCCYYVNGGSITYTEKYKEIRDRIQDQLNSLAAVULQNRARALDLLTAB
RGGTCLFLGEBCCYYVNGGSITYTEKYKEIRDRIQDGRAEELRNTGPWGLLSQWNFWILP
RGDNADIKGTPPEEISAAQPLLRPNSAGSS"
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                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

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1 (bases 1 to 2694)

Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.

The endogenous retroviral locus ERVWEI is a bona fide gene involve in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMeritux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69344 cedex 07, France
Location/Qualifiers
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Homo sapiens
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Matches 1133; Conserv
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2071 ACCAATCAGAGAGCTCACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGGCC
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/product="envel lope glycoprotein"
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/bb_xref="id="AAQ17663.1"
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TYCMTYFTQTGMSDGGGGYQDQAREKHYKEVISQLTRVTPPTQIVCLPSGIFFVCGTSA
TYCLMGSSESGNCFLSFLYPPWTIYTRQQLYNYTPPTQIVCLPSGIFFVCGTSA
YRCLMGSSESGNCFLSFLYPPWTIYTRQDLYNYTLQDQLNSLAAVLQNRRALDLLTAE
RGGTCLAGECCYTVNQSGIVTEKVKEIRDRIQRRARSLDLTAE
RGGTCLFGEBCCYTVNQSGIVTEKVKEIRDRIQRRABELRNTGPWGLLSQWMPWILP
FLGFLABECTTTGPTTTTGPTTRNLYNNFVSSRIERNTGPWGSKTKIYRRPLDRAPSP
RSDVNDIKGTPPREISAAQPLLRPNSAGSS"
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                                                                                  Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 2694)

Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,

Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.

The endogenous retroviral locus ERVWEI is a bona fide gene involve in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGGGAAGAATGCTTAGTATGTTAATCAATCTGGAATCTTACTTGAGAAAGTTAAAAGA
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Pred. No. 3e-304;
0; Mismatches 111; Indels
                                                                                                                                                                                                                                      Aallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (O'JUN-2002) Retrovirology Department,
CNRS-blowerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol type="genomic DNA"
/isolate="individual 71 allele A"
/db_xref="teaxon:9606"
/chromosome="7"
/map="721-q22"
/cell_type="PBMC's"
/cell_type="PBMC's"
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1959. .2694
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90.1%;
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                                                                          CCTCAGCCAATGGATGCCCTGGATTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATT
                                                                                                                                                 1891 AAGCAGTTAGAGCGGTCGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
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1771 GATCTACCGCAGACCCCTGGGCCTGCTAGCCCACGATCTGATGACATCAA
                                                                                                                                                                                                                                                                                                                                                              1831 AGGCACCCCTCCTGAGGAAATCTCAGCTGCACAACCTCTACTACGCCCCCAATTCAGCAGG
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                                                      CCTCAGCCAATGGATGCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATT
                                                                                                                            241 ITTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTTCCAGAAT
                                                                                                                                                                                                     301 TGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA
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/product=11_id=14Agl7604_i.1"
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/riggittstpfryypysgelytekvyesirbaygranglyspylyspylphypasp
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1 (Bases I to 2694)

Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.

The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology

Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
                      AF52056382 2694 bp DNA linear PRI 11-FEB-2004 Homo sapiens individual 71 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Direct (70-JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 77.9%; Score 1035.2; DB 9; Length 2694; Best Local Similarity 90.1%; Pred. No. 3e-304; Matches 113; Conservative 0; Mismatches 111; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="genomic DNA"
/isolate="individual 71 allele B"
/db xref="taxon:9606"
/chromosome="7"
/map="7421-q22"
/sex="male"
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1705. .1720
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284. .1900
note="syncytin"
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1959. .2694
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/organism="Homo sapiens"
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/note="African
                                                                                               AF520564.1 GI:33411096
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Homo sapiens (human)
Homo sapiens
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 56093)
Pauley,A.
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Unpublished (1996)
2 (bases 1 to 56093)
Waterston, R.
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Submitted (13-NOV-1996)
Genome Sequencing Center
Department of Genetics, Washingto
St. Louis, MO 63108, USA
e-mail: sapiens@watson.wustl.edu
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
          2610 TCCATAAGGCCAAGAACCCCAGGTCAGAGAACACGAGGCTTGCCACCATCTTGGGAG 2666
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Pred. No. 3.2e-304;
0; Mismatches 111;
                                                                                                                                                                                                                                                                    General Section 194629-A 81 13-DEC-2001;
Patent: WO 0194629-A 81 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
1. 56093
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                    DNA
                                                                                 AX329572 56093 bp
Sequence 81 from Patent WO0194629.
SX329572
AX329572.1 GI:18102550
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.1%;
Matches 1133; Conservative (
                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                          Homo sapiens (human)
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SOURCE
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                                                                                                 DEFINITION
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47898. .48115
/note="match to human 5' EST H62306 (NID:g1015138), bases
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/note="match to human 3' BST N29952 (NID:g1148472), bases
290-455, and 5' EST R12730 (NID:g765806)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(48787. .49405)
/rpt_family="ALU"
complement(49406. .49534)
/noces="match to human 3' EST R65794 (NID:g838432), bases
                                                                                                                                                            13794. .13877
/rpt_family="ALU"
13878. .13906
//gene="WUGSC:H_RG083M05.1"
/note="match to human 5' EST H41382 (NID:g917434), bases
30-58"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        omplement 45614. .45737)
note="match to human 3' EST H48898 (NID:9988738), bases
                                                              //pp. miminity - AUD
//post - 1379. 1379
/gone="WNGSC:H RG083M05.1"
/hote="match to human 5' EST H41382 (NID:917434), bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similarity to various SS-RNA virus polyproteins; pseudogene; region of matches and close matches to multiple human ESTs, see R68740 (NID:9842257)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt family="ALU"
18667. .19235
/note="match to human fetal brain 5' EST D61494
(NID:9970409), bases 1-255, and to human 3' EST R07476
(NID:9759399)"
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/note="match to multiple human ESTB, see N81064
(NID:91243765), H48897 (NID:9988737), and M78831
(NID:9273146)"
complement (47027. ,47318)
/rpt family="ALU"
complement (47365, 47782)
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/note="match to multiple human BSTB, see N30113
(NID:g1148633)"
39800. .40085
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/note="match to multiple human ESTs, see W37495
(NII:g1319089)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37316. .37489
/note="Grail prediction, score = 80"
/evidence=not experimental
complement (38938. .39224)
/rpt family="ALU"
39225. .39707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpc_family="ALU"

complement (42283. .42891)

/rpc_family="ALU"

complement (45474. .45613)

/rpc_family="ALU"

complement (45614. .45737)
                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="11"
complement (15618. .15907)
/rpt_family="ALU"
17227. .17522
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complement(40632, 40924)
/rpt_family="ALU"
42891)
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/rpt family="ALU"
complement(48406. .48584)
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/rpt_family="ALU"
complement(14110. .14137)
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complement(40247. .40538)
/rpt_family="ALU"
                        .12907
                          complement (12612. /rpt_family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19550. .19670
/rpt_family="ALU"
21507. .37303
                                                                                                                                              143-266"
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/ Drotein id="AAB46346.1"

/ Drotein id="AAB46346.1"

/ Drotein id="AAB46346.1"

/ Linelation="KRLENIQKTEVAFSEAVWMQPSVVLLDDLDLIAGLPAVPEHEH
SPDAGGKCELLCNVIKKLDCDINKFTDLDLQHVAKETGGFVARDFTVLVDRAIHSRL
SRQSISTREKLVLTTLDFQKALRGFLPASLRSVNLHKPRDLGMDKIGGLHEVRQILMD
TIQLPAKVCLKKEKYPELFANLFRQKARGTLLAYGFGTGKTLLAGVTARRESMNFTSV
KGPELLSKYIGASEQAVRDIFIRAQAAKPCILFPDEFESIAPRRGHDNTGYTDRYVNQ
LLTQLDGVRGLGGCYVTAATSRPBLLDPALLRRGRLDKCVYCPFPDQVTISYLESKTQ
QMLASFLVSRLEILNVLADSSLPLADDVDGHVASYTDSFTGADLKALLYNAQLEALHG
MLLSKMSBILDDESKFNMYRLYFGSSYESELGNGTSSDLSSQCLSAPSSMTQDLPCVP
GKDQLFSQPPVLRTAGGSCGELTQBCRDGNGTSSDLSSGCLSAPSSMYQPEPV
KTRLAISQSHLMTAAGHTRFSISEDDWKNFAEL"
                                                                                                                                                                                         This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 9788K. For references see: Shizuya et al., Proc. Natl. Acad. Sci. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996).
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/gene="WUGSC:H_RG083M05.1"
/note="match to human 5' EST N22627 (NID:g1130501), bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="WUGSC:H_RG083M05.1"
note="match to human 3' EST H75782 (NID:g1049794), bases
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This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                        NEIGHBORING SEQUENCE INFORMATION:

He orientation of this clone is unknown. Actual start of this clone is at base position 1 of H_RG083M05; actual end is at 56093 of H_RG083M05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="WUGSC:H_RG081M05.1"
/note="ATPPase; atrong similarity to peroxisome
blosynthesis protein PAS1 (PID:g1172019); coded for by
human cDNA C04279 (NID:g1467530)
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/gene="WUGSC:H_RG083M05.1"
/note="match to human 5' EST H75921 (NID:g1050050),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (4948. 5130)
/rpt family="ALU"
complement (6581. 7133)
/rpt family="L1"
complement (7767. 8037)
/rpt family="ALU"
complement (8186. 8472)
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'organism="Homo sapiens"
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8473. .8625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone contains STS 8WSS1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="7"
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Homo sapiens BAC clone CTB-10G5 from 7q21-7q22, complete sequence.
AC007566
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AATCATCTATTGCCTGAGAGCACAGGGGAAGGACAAGGATTGGGATATAAAACTCAGGCA
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Unpublished (2001)
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Sulston,J.B. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Waterston, R.H.
Direct Submission
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                           complement (49638. .49672)
/rpt family="ALU"
complement (49674. .49890)
/note="match to human 3 ' EST N29952 (NID:g1148472) and
EST N29938 (NID:g1148458), sequences are from opposite
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                                                                                                                                                             Complement (49698 . 51806)
/gene="WUGSC:H_RG083M05.2"
complement (join (49698 . 49888,51575. .51806))
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R65891 (NID:g838529), R65794 (NID:g838432) and R65794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGAACCTGTTTATTTTT
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Pred. No. 3.2e-304;
0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (51576. 51758)
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/note="Grail prediction, score = /evidence=not_experimental
complement (52562. 52329)
/rpt_family="Li"
55557. 55843
                                                                                                                                          ends of the same clone" complement (49698. .5180
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Best Local Similarity 90.1%;
Matches 1133; Conservative
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COMMENT

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note="match to EST AA149693 (NID:g1720635) zn99d06.rl"
1542. .3628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match to EST AA425526 (NID:g2106267) zw48b03.rl"
3540. .3628
/note="similar to Mus musculus EST BB253526
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                                                                                                                                                                                                                                                                                                                                                                   (NID:91720635) zn99d06.rl"
CTB-10G5 contains the entire sequence of CTB-83M5.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="match to EST AU123510 (NID:g10948226)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="match to EST AV686676 (NID:g10288539)"
                                                                                                                                                                                                                                                                       /rpt_family="L1"
2248. . 2388
2248. . 2388
2248. . 2387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="match to EST AV686676 (NID:910288539)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NID:g10948226)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match to EST AV686676 (NID:g10288539)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="match to EST AU123510 (NID:g10948226)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="match to EST BG766882 (NID:914077535)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NID:914620366)"
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/note="match to EST BE299708 (NID:g9183456)"
3719. .3785
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match to BST BG766882 (NID:g14077535)"
2248. .2387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="match to EST BI160365 (NID:g14620366)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="match to EST AW579261 (NID:g7254310)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="match to EST BE272564 (NID:g9146913)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="match to EST BE299708 (NID:99183456)"
                                                                                                                                                                                                                                                                                                                                                                                                                     (NID: 97254310)"
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(NID:910678674)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to Homo sapiens EST BF758865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match to EST BI1603653542. .3609
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/note="match to EST AW579261
2248. .2387
                                                                                                                                                                                                                                                                                                                                                                     'note="match to EST AA149693
                                             1. .149194
|organism="Homo sapiens"
|mol_type="genomic DNA"
|db_xref="taxon:9606"
|chromosome="7"
                                                                                                                                                                                                                          clone lib="CITB-978SK-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="MalR"
3108. .3392
/rpt_family="Alu"
3540. .3628
                                                                                                                                                                                                     clone="CTB-10G5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NID:912106765)"
                                                                                                                                                                            /map="7q21-7q22"
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                                FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone CTB-10G5 is from the first release of the human BAC library CTB-978SK-B. The library contains cloned DNA from the male CIFB-978SK cell into 978SK. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1922); U-J. Kim et al., Genomics 34:213-8 (1996). This clone is available from Research Genetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-OCT-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 5 (bases 1 to 149194) Waterston, R.H.
                                                                                                                              Submitted (16-NOV-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 53108, USA 6 (base 1 to 149194) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mo 63108, USA 8 (bases 1 to 149194) Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                        Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RFS-911H5, 200 base pair
overlap. Actual ext of this clone is at base position 195 of
CTB-10G5; actual end is at base position 150532 of CTB-10G5.
                                                                                                                                                                                                                                                                  Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA 7 (bases 1 to 149194) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_RG010G05
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                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                    Direct Submission
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	RESULT 35  RESULT 35  LOCUS  LOCUS  LOCUS  LOCUS  LOCUS  LOCUS  AF520485.2  AF520486.1  REFERENCE  SOURCE  ACCESSION  REFRENCE  ACTOR Sapiens individual 148 allele A, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.  ACCESSION  AF520486.1  AF520486.1  AF520486.1  AF520486.1  GI:33410940  REFRENCE  SOURCE  SOURCE  AMMENTIALS  REFRENCE  I (Dases 1 to 2634)  AUTHORS  Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Mallet, F., Bouton, O., Duret, L. and Mandrand, B.  TITLE  TITLE  In hominoid placental physiology  JOURNAL  Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)  AUTHORS  Mallet, F., Bouton, O. and Oriol, G.  AUTHORS  AUT
misc_feature 3719. :3785  misc_feature 3719. :3785  misc_feature 3719. :3785  misc_feature 3719. :3785  misc_feature 3719. :3785  misc_feature 3719. :3785  misc_feature 3862 :3862  misc_feature 3862 :3862  misc_feature 4731 :3862 :3862  misc_feature 5715. :3860  misc_feature 6715. :3860  misc_feature 771.3%; Score 1035.2; DB 9; Length 149194;  metches 1133; Conservative 0; Mismatches 111; Indels 13; Gaps 2;  misc_feature 5715. :3860  misc_feature 6715. :3860  misc_feature 771.3%; Score 1035.2; DB 9; Length 149194;  matches 1133; Conservative 0; Mismatches 111; Indels 13; Gaps 2;  misc_feature 6715. :3860  misc_feature 771.3%; Score 1035.2; DB 9; Length 149194;  matches 1133; Conservative 0; Mismatches 111; Indels 13; Gaps 2;  misc_feature 771.3%; Score 1035.2; DB 9; Langth 149194;  matches 1133; Conservative 0; Mismatches 111; Indels 13; Gaps 2;  misc_feature 771.3%; Score 1035.2; DB 9; Langth 149194;  matches 1134; Mill	181   CCTCAGCCAATGGACCCTGCACTCCTTTAGGACCTCTAGCAGCTATAATATT   240   181   CCTCAGCCAATGGATGCCTGGAATTCTCCTCTTTAGGACCTCTAGAGCTATAATATT   84747   84806   CCTCAGCCAATGGATTCTCCCCTTCTTTTAGAGCTCTTCCAGAAT   84687   84746   GCTACTCTTTTGGACCTGTATCTTTCTTGTTTTTTTTTCTCCTTCCAGAAT   84687   84687   84687   84687   84687   84688   84689   84686   GGAAGCTGTAAAACTAAACTCTTTGAATTGACTTTCCAGAAT   84689   84686   GGAAGCTGTAAAACTAAAACTAAAATGAACTCCTTTGATAACTTAAACATTAAACATAAAAATAAAAATAAAAATAAAAATAAAAATAAAAATAAAA

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AF520492
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Mallet,F., Bouton,T., and Mandrand,B.
The endogenous retroviral locus ENVWEI is a bona fide gene involve in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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                                                                                                                                                                                                                           AGCTGGGAAGGTGACCACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTG
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AATCATCTATTGCCTGAGAGCACAGGGGAAAGGACAAGGATTGGGGATATAAACTCAGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCCATTGCCACTCCCGATCAGGCTAAAGGCTTGCCATGTTCCTGCATGGCTAAGTGCC
                                                                                                                                                                                                                                                                                             CATGCTATTTCACTCTATTAAATCTTGCAACTGCACTCTTCTGGTCCATGTTTCTTACGG
                                                                                                                              ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC
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Mallet,F., Bouton,O. and Oriol,G.
Direct Submitssion
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CURS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
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LVGPLVSNLBITHTSNLTCVRFSNTTYTTROCITRWTYPPTQLVCBFSGFFVCGTSA
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Mammalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mummalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucctte,G. Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEI is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
14757826
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 2694)
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWEl is a bona fide gene involved
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            Mallet,F., Bouton,O. and Ollet,C.,C.,C. Direct Submission.

Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
Submitted (07-JUN-2002) Retrovirology Department, UMR 2142
CRRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69164 cedex 07, France
Location/Qualifiers
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Pred. No. 9.2e-304;
0; Mismatches 112; Indels
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                                                                                                                                                                         /organisma"Homo sapiens"
/mol type="genomic DNA"
/isolate="individual 30 allele
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/chromosome="7"
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/note="splice acceptor site"
1959. .2694
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/note="splice acceptor site"
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/cell_type="PBMC's"
/note="caucasian
endogenous_virus: HERV-W"
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/note="syncytin"
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Best Local Similarity 90.1%;
Matches 1132; Conservative
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                       AUTHORS
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1 (bases 1 to 2694)
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GATCTACCGCAGACCCCTGGACCGGCCTGCTAGCCCACGATCTGATGATGACATCAA
                                     541 GGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
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                         AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG
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Homo sapiens (human)
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                                        Mallet,F., Bouton,O. and Oriol,G.
Direct Submission
Submitted (O'JUN-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Superieure de Lyon - 46 allee
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9; Length 2694;
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  in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
14757826
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Pred. No. 9.2e-304;
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                                                                                                                                /note="splice acceptor site"
284. 1900
/note="spncytin"
/note="spncytin"
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/prodon_t="envelope glycoprotein"
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Best Local Similarity 90.1
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Homo Bapiens individual 45 allele B, envelope glycoprotein gene, complete cds, and 3' long terminal repeat, complete sequence.
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                                    AAGCAGTTAGAGCAGTTGTCAGCCAACTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA
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Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B. The endogenous retroviral locus ERVWEl is a bona fide gene in hominoid placental physiology Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004) 1475/826
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/mol type="genomic DNA"
/isolate="individual 37 allele B"
/db_xref="taxon:9606"
/chromosome="7"
/map="7921-q22"
/cell_type="PBMC's"
/cell_type="PBMC's"
/note="endogenous_virus: HERV-W"
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protein id="AAQ17576.1"
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RGGTCLFLGEECCYYVNQSGIVTRKVSRIEAVKLQMBPKMQSKTKIYRRPLDRPASP
RSDVNDIKGTPPEEISAAQPLLRPNSAGS"
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.

1 (bases 1 to 2694)
Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G.,
Bonnaud, B., Lucotte, G., Duret, L. and Mandrand, B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
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Pred. No. 9.2e-304;
0; Mismatches 112; Indels 13; Gaps
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- 46 allee
                                                                                                                                                                                                                                                   Mallet, F., Bouton, O. and Oriol, G.
Direct Submission
Submitted (OrJUN-2002) Retrovirology Department,
CNRS-blomerieux, Ecole Normale Superieure de Lyon
d'Italie, Lyon 69364 cedex 07, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 2694
| organism="Homo sapiens" |
| nol type="genomic DNA" |
| isolate="individual 45 allele B" |
| db xref="taxon:9606" |
| chromosome="7" |
| sex="male" |
| sex="male" |
| cell Lype="PBMC's" |
| note="endogenous_virus: HERV-W"
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/note="splice acceptor site"
284. .1900
/note="syncytin"
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1959. .2694
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Best Local Similarity 90.1%;
Matches 1132; Conservative C
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                                                                     REFERENCE
AUTHORS
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Human end Human end 3' pol ge Human end

Complete

Aax25660 Human end Aax35210 3' pol ge Aax5561 Human end Aaa59211 5' non co Aah20069 HERV-W en Aai14608 Probe #45 Aba5637 Human bor Aba5839 Probe #46 Aba45822 Brobe #46 Aba45829 Brobe #46 Aba45829 Probe #46 Aba64516 Human bor Ab629670 Human Bra Ab629670 Human gen Aas64516 Human gen Aas6364 DNA encod Aas65964 DNA encod Aas65964 DNA encod Aas65964 DNA encod

Acn44334 Human gen Aax25669 Human end

Ads31352 Human gen

Ade09587 Novel DNA Abn97930 Human ret

OM nucleic

Run on:

Sequence:

Title: Perfect

Searched:

Database

Result No.

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/product= "Encodes protein AAW71069"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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AAX25669
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ADE09587
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AAK04516
ABS29670
AAI04422
ABS04589
AAS77313
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AAX25661
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AAH20069
AA114608
AAA135980
ABA583378
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Aax29704 Clone 5M6
Adg14849 MSRV as 880
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Aaz59468 Human sec
Adc38776 Human cDN
                                                                                                                      February 21, 2005, 06:25:25; Search time 685.525 Seconds (without alignments) 11476.370 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                    4390206 seqs, 2959870667 residues
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New nucleic acid from retroviruses - useful for diagnosis, prevention and

WPI; 1998-322732/28.

P-PSDB; AAW71069.

Aad24195 Human syn Aaf55630 Nucleotid Aas84210 DNA encod

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                                    GCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGT
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P-PSDB; AAW99554.
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                                                     The present sequence represents a multiple sclerosis (MS) associated retrovirus (MSRV) genomic fragment used in the method of the invention. The invention provides complete or partial genomic sequences of the MSRV-1 pol gene, gag gene and env gene, and polypeptides encoded by these genes. The invention also provides antibodies raised against the polypeptides. The genomic sequences, polypeptides and antibodies are also claimed useful for diagnosing infection by MS and rheumatoid arthritisassociated viruses, and also for prevention and treatment of infection with these viruses
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                                   Disclosure; Page 187-188; 286pp; English
             of, e.g. multiple sclerosis.
                                                                                                                                                                                  Seguence 1329 BP; 346 A; 352
                treatment
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CACTCTATTTCACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGG
                                                                      TGGGTTTGTCCTAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTCTCTTCCATGAC
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Jolivet-Reynaud C, Mandrand
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97US-00979847.
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Komurian-Pradel F,
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                         This sequence represents clone 5M6 from a novel multiple sclerosis related virus type 1 (MSRV1). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis. (Updated on 27-ANG-2003 to correct OS field.) (Updated on 17-OCT-2003 to standardise OS field)
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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New isolated or purified nucleic acid associated with multiple sclerosis and/or rheumatoid arthritis, useful for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample.
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Jolivet-Reynaud C, Mandrand
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"^MURIAN-PRADEL F.
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GARSON J A.
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Komurian-Pradel F,
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arthritis. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating multiple sclerosis and/or rheumatoid arthritis. The present sequence is used in the exemplification of the invention.
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stomach, lung, prostate, pancreas, carcinoma, antitumour, cancerous,
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                         The invention relates to an isolated or purified nucleic acid from a virus associated with multiple sclerosis and/or rheumatoid arthritis.

C wiltiple sclerosis-associated virus (MSRV)-1. The nucleic acids comprise poly, gag or reverse transcriptase genes (or their fragments) encoding the proteins or reverse transcriptase genes (or their fragments) encoding the proteins or defined peptides (including immunodominant peptides).

CC derecting a virus associated with multiple sclerosis or rheumatoid arthritis, a prime for the amplification by polymerisation of a nucleic acid of a viral material associated with multiple sclerosis or rheumatoid arthritis, a polymeptide exhibiting an inhibitory activity from MSRV, and an antibody directed against the MSRV-1 virus obtained by correcting a human or animal body or calls with an immunogenic agent consisting of the antiganic polypeptide defined above. The nucleic acids are useful for detecting a biological sample a virus associated with multiple sclerosis or rheumatoid arthritis. The present cassociated with multiple sclerosis or rheumatoid arthritis. The present cassociated with multiple sclerosis or rheumatoid arthritis. The present sequence is a claimed MSRV-associated sequences as cacurately determined. Note: The SEQ ID numbers for the sequences as claimed many more them acid ont match the SEQ ID numbers in the main body of the patent do not match the SEQ ID numbers in the main hold or an antiboned in the main body of the patent do not match the SEQ ID numbers in the main hold or an antiboned in the main hold or an antiboned in the main hold or an antiboned in the main hold or an antiboned in the main hold or an antiboned in the main hold or an antiboned in the main hold or an antiboned in the main hold or an antiboned in the main hold or an antiboned in the main hold or an antiboned in the main hold or an antiboned in the main hold or an antiboned in the main hold or an antiboned in the main hold or an antiboned in the main hold or an antiboned will be antiboned be an
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larity 98.0%; Pred. No. 0;
Conservative 0; Mismatches 27; Indels 0
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The present invention describes a method (MI) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in activity and can be used to anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-0CT-2000; 2000US-0237172P.
02-0CT-2000; 2000US-0237173P.
02-0CT-2000; 2000US-023724P.
02-0CT-2000; 2000US-0237294P.
02-0CT-2000; 2000US-0237295P.
03-0CT-2000; 2000US-023734FP.
03-0CT-2000; 2000US-0237345P.
                                                                                                                                 2000US-0234509P
2000US-0234509P
2000US-0234507P
2000US-0234923P
2000US-0234924P
2000US-0234924P
2000US-0235082P
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03-0CT-2000; 2000US-0237606P.
03-0CT-2000; 2000US-0237608P.
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2000US-0234009P.
2000US-0234034P.
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Weaver Z;
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20-SEP-2000;
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26-SEP-2000;
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28-SEP-2000;
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Soppet DR,
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37486 AAGCAGTTAGAGCGGTCGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA 37545
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prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous call carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour
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                                                                                                                                            TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTT
                                                                                                                     13; Gaps
                                                                    Sequence 56093 BP; 16164 A; 12346 C; 10702 G; 16881 T; 0 U; 0 Other;
                                                                                          Query Match
Best Local Similarity 90.1%; Pred. No. 0;
Matches 1133; Conservative 0; Mismatches 111; Indels 13;
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                                                                                                                                                                                                       CITGAGCTGAGCTTTCGCTCGCCATCCACCACTGCTGTTTGCCGCCACCGCAGACCCGCC 37965
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                                                                                                                                                                                      The present invention describes isolated polynucleotide sequences (I), which encode polypeptides (II) with biological activity. Also described: (II) a vector comprising (I); (2) an expression vector comprising (I); (3) a special genetically engineered to comprise (I) which is operatively associated with a regulatory sequence that modulates expression of (I) in the host cell; (4) a polypeptide (II) encoded by (I); (5) a composition comprising the polypeptide of (4) and a carrier; (6) an antibody directed against the polypeptide of (4) and a carrier; (5) a composition of (4) in a sample; (8) identifying a compound that binds to the polypeptide of (4) in a sample; (8) identifying a compound that binds to the polypeptide of (4); (7) detecting (I) or the polypeptide of (4); (9) producing the polypeptide of (4); and (10) a collection of polynucleotides comprising at least one of the polynucleotide sequences (I). The polynucleotides (I) can be used as hybridisation probes, oligomers or primers, for chromosome or gene mapping, for the recombinant
                          GCTGACTTCCATCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGT 1020
                                                                              ACCCATTGCCACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCC 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                 '; genetic engineering; hybridisation probe; oligomer; mapping; gene mapping; recombinant protein production;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides, useful as hybridization probes, oligomers or primers, for chromosome or gene mapping, for the recombinant production of proteins, and for generating antisense DNA or RNA.
                                                                                                                                                                                                                                          | TCTGTGAGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTTGGGAAG 1257
                                                                                                                                    TGGGTTTGTCCTAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTCTTCCATGAC
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human; gene; ss.
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production of proteins, and for generating antisense DNA or RNA. The present sequence represents a human contig polynucleotide sequence, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                        AATTTGAGATCGAATATAATGTAGAGCAGAGGACCTTCAAAACACTGCACCCTGGGGCCT
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                                                                                                                                                           Gaps
                                                                                                                   Length 9502;
                                                                                                                                                         33;
                                                                              G; 2263 T; 0 U; 1 Other;
                                                                                                               Score 1029.4; DB 10; Lengt
Pred. No. 0;
0; Mismatches 129; Indels
                                                                                BP; 2813 A; 2433 C; 1992
                                                                                                                   77.5%;
87.9%;
                                                                                                                                       Best Local Similarity 87.9
Matches 1178; Conservative
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protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was used to illustrate the invention
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involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at Itp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (ix) as a biochip; (x) for diagnosing carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent
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                        4390 CAAGAACCCCAGGTCAGAGAACAAAAGGCTTGCCACCATCTTGGAAGCGGCCTGCTACCG
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                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 910; Opp; English.
                                                                                                                                                                                                                                                                                                                                      Human genomic sequence hCG1748307.
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                         Homo sapiens
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17-MAY-2000;
                                    30-AUG-2001
     Human
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that affect the activity of the DITHBs, by expressing inactive genome, crapplementaring the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder.

Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma, leukacemia, autoimmune disorders, and respiratory disorders. Additionally, (I) may be used to produce the DITHPs, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) and its complementary sequences may also be used as DNA probes in disgnostic sangles, and therefore which patients may be in need of restorative camples, and therefore which patients may be in need of restorative camples, and therefore which patients may be in the production of antibodies against DITHPs and in assays to identify modulators of DITHP expression and activity. The anti-DITHP antibodies and antagonists may also be used as antisposit and activity. The anti-DITHP antibodies and antagonists may be used to down regulate expression and activity. The anti-DITHP copression and activity. The anti-DITHP antibodies and antagonists may also be used as diagnostic agents for detecting the presence of DITHPP is samples (e.g. by enzyme linked immunosorbant assay the profile.). Assalloge-Assalloge represent human diagnostic and therapeutic contemps.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC; Chen A, D'sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE, Dufour GE; Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL, Liu TF; Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Daffo A; Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W; Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics.
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                                                                                                             Human; receptor; diagnostic; therapeutic; gene therapy; vaccine; cell proliferative disorder; Crohn's disease; lymphoma; leukaemia; acquired immune deficiency syndrome; AIDS; autoimmune disorder;
                                                                diagnostic and therapeutic polynucleotide (DITHP) #17.
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2000US-0203785P
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2000US-0184813P.
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1500 GATCCACCGTGGACCCTGGACCGGCCTGCTAGCCCCATGCTCGATGTTAATGACATTGA 1559
                                                         The present sequence represents the nucleotide sequence corresponding to the 3' env region and long terminal repeat sequences from clone CL6 of Multiple Sclerosis retrovirus (MSRV-1). The specification describes a long terminal repeat (ITR)-RUS region which encodes the expression of a MSRV-1 protein. This is unusual for LTRs, in particular in the RUS region. The sequence includes CAAT and TATA signals which are present in the U3 and R regions and are not directed towards the CDS indicated in the features table. Probes and antibodies to the MSRV-1 retrovirus protein and encoding polymuclectide sequences are used to detect the presence of MSRV-1 retrovirus in a biological sample. (Updated on 06-AUG-2003 to correct OS field.)
to detect the presence of MSRV-1 retrovirus in a biological
                                                                                                                                                                                                                                                                                                                                                                                       1200 AGGAGAAGAACGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAAGTTAAAGA
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Pred. No. 2.1e-243;
0; Mismatches 63;
                                         English
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92.8%;
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Matches 812; Conservative
                                       Disclosure, Fig 2; 23pp;
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                                         TCCATGACCCACGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATT
                                                                                                                                             TCCGTGACCCCACGACTTCTAATAGAGCTATAACACTCACCGCCACGGCCCAAGATTCCATT
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                                                                                   1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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       1860 AATCATCTATTGCCTGAGGGCACAGGGGGGGGGACAAGGATCGGGATATAAACCCAGGCA 1919
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                                               TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                                                                                                                                                                                                                                                                                                               Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7974 BP; 2034 A; 2017 C; 2123 G; 1800 T; 0 U; 0 Other;
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llarity 85.8%; Pred. No. 1.2e-242;
Conservative 0; Mismatches 126;
                                                                                                                                            875
                                                                                                                        CACTCTATTTCACTCTATTAAATCATGCAACTGCA
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                                                                                                                                                                                                                                                                                                                                                                          seq id 9936
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Matches 937; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003099974-A1.
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Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis; cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic disorder; neurological disorder; gastrointestinal disorder; transport disorder; connective tissue disorder; dasorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder; disorder;
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                                                                                        CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTTAGGACCTCTAGCAGCTATATAT
                                                                                                                                                                                   TTTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTTTCCAGAAT
                                                                                                                                                                                                                                                                            TGAAGCTGTAAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA
                                                                                                                                                                                                                                                                                                                                                                     361 AATCTACCGTGGACCCGCCTGGCCTGCTAGACTATGCTTGATGATGACATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 AGTCACCCTCCCGAGGAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG
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ACC46747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human embryogenesis associated proteins (EMBRY) and nucleic acid molecules encoding such proteins. EMBRY sequences are useful for screening modulators useful for treating or preventing disorders associated with abnormal expression of EMBRY. The disorders treated include reproductive disorders such as infertility, endometriosis, endometrial or ovarian tumour; autoimmune/inflammatory disorders uch as equired immune deficiency syndrome (AIDS), allergies, contact dermattiis; disorders of the placenta such as preeclampsia, abruptio placentae etc. Sequences of the invention are also useful for analysing a proteome of a tissue or a cell type. EMBRY proteins are useful as immunogens for preparing antibodies. Polynucleotides of the invention are useful for creating knockin humanised animals or transgenic animals to model human diseases. They are also used in gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGAGAAGAATGCTGTTATTATGTTAATCAATCCAGAATTGTCACTGAGAAGTTAAAGA 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides of human embryogenesis associated proteins for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                     Human; embryogenesis associated protein; AIDS; reproductive disorder; infertility; endometriosis; endometrial tumour; inflammatory disorder; autoimmune disorder; acquired immune deficiency syndrom; transgenic; ovarian tumour; contact dermatitis; placenta disorder; preeclampsia; ovarian tumour; contact dermatitis; placenta disorder; preeclampsia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modulators useful for treating or preventing disorders e.g. endometriosis, infertility, allergy, preeclampsia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Mature EMBRY-2 protein"
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Pred. No. 1.4e-240;
                                                                                                                                                                                                                                                                                                                                                                     /product= "EMBRY-2 protein"
64. 123
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124. 1689
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence is human EMBRY-2 CDNA
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                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Best Local Similarity 93.0%;
Matches 812; Conservative
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                               (first entry)
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                                                                            Human EMBRY-2 CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
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28-MAR-2001; 2001US-0279619P.
29-MAR-2001; 2001US-0280067P.
29-MAY-2001; 2001US-029108P.
17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-0299428P.
20-JUN-2001; 2001US-0299428P.
                 27-MAR-2002; 2002WO-US010056
                                                           (INCY-) INCYTE GENOMICS INC.
          05-DEC-2002
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The invention relates to novel human diagnostic and therapeutic conjugated dithp (ACC46080-ACC46749) and to their encoded polymucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHP; ABR41186-ABR41812). The invention also relates to polymucleotide sequences at least 90% identical to the dithp cDNA sequences of the invention; recombinant whost cells and transgenic organisms comprising a dithp nucleic acid sequence; the transgenic organisms comprising a dithp nucleic acid sequence; the crecombinant production of DITHP proteins; antibodies specific for DITHP proteins antibodies specific for DITHP proteins and protein sequences; methods of detecting dithp nucleotide and protein sequences; methods of some seasons the toxicity of test compounds using a dithp hybridisation of probe. Dithp nucleic acid sequences and DITHP proteins may be used in the assessing the toxicity of test compounds using a dithp hybridisation continuation of a wide variety of conditions including cancer and other cell continuates in the amplituding cancer is mad other cell continuations including cancer and other cell continuations in flammatory disorders; ransport disorders; neurological disorders; pastrointestinal disorders; ransport contess; and connective tissue disorders. They may also be used to disorders; neurological disorders. They may also be used to cell type and connective tissue disorders. They may also be used to cell type and to induce antibodies. They may also be used to continually useful in somatic or germline gene therapy of the disorders additionally useful in somatic or germline gene therapy of the disorders and primers, in genotyping and identification of individuals, in toxicological testing, and in transcript imaging. The present sequence represents a dithp cONA and an invention of the protein and the protein and madels of the protein accorders and accorders and accorders and accorders and accorders and accorders and accorders and accorders and accorders and accorders and accorders and accor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.
Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
DuGour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 668; 591pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-129518/12.
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16; 56.3%; Score 747.6; DB 8; Length 2046; 86.5%; Pred. No. 2.9e-234; ive 0; Mismatches 122; Indels 16; Sequence 2046 BP; 587 A; 494 C; 391 G; 566 T; 0 U; 8 Other; 0; Best Local Similarity 86.5 Matches 885, Conservative Query Match

257 CCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTTTCCAGAATTGAAGCTGTAAAGCTA 316

1154 1460 977 TTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGTACCCATTGCCACTCCC 1036 GATCAGGGTAAAAGGCTTGCCCATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCCTAATA 1096 916 976 736 496 616 930 676 436 AGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGTATCTGTGAGGCCAAG AGAGCACAGCGGAAGGACAAGGATTGGGATATAAACTCAGGCATTCAAGCCAGCAACAG 1097 GAACTGAACACTGGTCACTGGGTTCCATGGTTCTCTT-CCATGACCCACGGC-TTCTAAT CTCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTCCAGAATTGAAACTGTAAAACTA AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGGGAAGGTGACC ACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCCAATCATCTATTGCCTG GTTCGCCATCCACCACTGCTGTTTGCCACCGTCACAGACCCGCTGCTGACTTCCATCCCT CAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAAAATCTACCGTGGACCC CTGGACCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGAAGTCACCCCTCCCGAG CAACCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTCACTCTATTTCACTCT GAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGGAAGCAGTTAGAGCAGT TGG 1276 1155 1274 677 737 797 857 1161 917 1221 1037 1461 1518 557 871 571 317 631 377 691 437 g 셤 g d 엄 g g ò ద ò 셤 ò g à ò ò ò a ઠે δ ò ò ð d ò g ò g g δ

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2715 ACCAATCAGAGGCTCACTAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCC
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                                                                                                                                                  301 TGAAGCTGTAAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA
                                                                                                                                                                                                                           361 AATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA
                                                                                                                                                                                                                                                                                                                                                                                   481 AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGGTTTTCCTGTTGAGA
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                                                                       241 TTTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel human secreted proteins encoded by polynucleotides isolated from human adult testes, adult brain, adult blood or adult placenta, or murine adult bone marrow or thymus cDNA libraries. The products of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth activity, activity, activity, insue growth activity, haematopoiesis regulating activity, tissue growth activity, haemostatic activity, receptor/ligand activity, and themour and thromodylvic activity, receptor/ligand activity, and tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for
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                                                                                                                                                    Secreted protein; testes; brain; blood; placenta; human; murine; thymus; bone marrow; treatment; prevention; nutrition; cytokine; immune; vaccine; cell proliferation; cell differentiation; suppressor; tumour inhibition; haematopoiesis regulator; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; tumour; cadherin; tumour invasion suppressor; gene therapy; tissue growth; ss.
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Pred. No. 5.7e-229;
0; Mismatches 69;
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                                                                                                                   Human secreted protein AJ172_2
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98US-00080478.
98US-00175928.
  standard; cDNA; 2946
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Local Similarity 90.7%;
New 794; Conservative
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC.
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Treacy M;
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20-OCT-1998;
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Merberg D,
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Matches
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ANCTEGGAAGGTGACCGCATCCATCTTAAACATGGGGCTTGCAACTTAGCTCACACCCG
                                                                                                                                                                                                                                                                                        721 AATCATCTATTGCCTGAGAGCACAGGGAAAGGACAAGGATTGGGATATAAACTCAGGCA
                                                           GGGTGGACTGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
                                                                                                                                                                                                             ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene; immune disorder; severe combined immunodeficiency; SCID;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA encoding a secreted protein #63.
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96US-00635311.
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96US-00721798
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13-JAN-1997;
10-APR-1997;
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09-JUL-1996;
26-JUL-1996;
23-AUG-1996;
27-SEP-1996;
27-SEP-1996;
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19-APR-1996;
07-JUN-1996;
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                                                                                                                                                                                                                                                                                                          This is the human secreted protein AU172 2 nucleotide sequence, obtained from a human adult testes cDNA library. The invention relates to secreted human and murine proteins. The polymucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Detecrion of the levels of the proteins can be used for the diagnosis of e.g. pre-eclampsia, placental pathology or cancer. Agents which modulate the expression or function of the proteins may be used for treating a neoplastic disease and inhibiting metastasis. Other suggested activities include nutritional activity (e.g. in feeds), cytokine and cativities include nutritional activity (e.g. in feeds), cytokine and cativity and suppressing activity, haemcostaic activity, themcostaic activity, chemcitic activity, haemcostaic and thrombolytic activity, chemcitic/chemckinetic activity, haemcostaic and thrombolytic activity, creeptor/ligand activity, and tumour inhibition activity. The invasion suppressor activity, and tumour inhibition activity. The propries are also stated to be useful for gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATTTGAGATCGAATATAATGTAGAGCAGAGGACCTTCAAAACACTGCACCCTGGGGCCCT
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                                                                                                                                                                                                                   New polynucleotides encoding secreted cDNA libraries, used to develop products for the diagnosis and treatment of neoplastic disease.
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                                                                                                        Evans C;
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                                                                                                        Collins-Racie LA,
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Pred. No. 5.7e-229;
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                                                                                                      Lavallie ER,
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90.7%;
             98US-00080478.
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                                                                   GEMY ) GENETICS INST INC.
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Best Local Similarity 90.7
watches 794; Conservative
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                                                                                    Jacobs K, Mr
               18-MAY-1998;
                                 20-OCT-1998;
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                                                                             AAGCAGTTAGGAGCAGTTGTCAGCCAACCCCCAACAGTACTTGGGTTTTCCTGTTGAGA
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                                                         agtcaccccccccgaggaaatctcactgcacaacccctactacactccaattcagtagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, syncytin; preeclampsia; gestational trophoblast disorder; choriocarcinoma; hydatiform mole; placental site tumour; abortion; envelope gene; human endogenous defective retrovirus; HERV-W; ss.
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/product= "Syncytin"
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C protein or BD127 16 protein. The polynucleotides are useful for
expressing recombinant proteins for analysis and are also useful as
chromosome markers or tags to identify chromosomes or to map related
continue. The proteins are useful as amino acid supplement, carbon
positions. The proteins are useful as amino acid supplement, carbon
c continued immunodeficiency (SCID); autoimmuno disorders (e.g. severe
c combined immunodeficiency (SCID); autoimmune disorders (e.g. multiple
c continued immunodeficiency (SCID); autoimmune disorders (e.g. multiple
c continued is systemic lupus erythematosus, rheumacid arthritis), allergic
reactions (e.g. asthma), myeloid or lymphoid cell deficiencies,
c sclerosis, systemic lupus erythematosus, rheumacid arthritis), allergic
c cagulation disorders, inflammatory diseases (e.g. systemic inflammatory
c peripheral neuropathy. Alzheimer's diseases (e.g. systemic inflammatory
c response syndrome (SIRS), ischaemia-repertusion injury, Crohn's disease),
c anaphylaxis and hypersensitivity. Proteins are also useful for inducing
t tumour immunity, for inducing bone, cartilage, tendon, ligament and/or
c nerve growth or regeneration, for proliferating neural cells and for
c regenerating nerve and brain tissue, for inducing fertility and for
c inhibiting tumour growth. Proteins are also useful as chemokine for
mammalian cells (e.g., monocytes, fibroblasts, neutrophils), and also
c useful as inhibitors of receptor/ligand interactions. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGGGAAGAATGCTGTTATTATGTTAATCAATCCGGAATCGTCACTGAGAAGTTAAAGA 2186
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                                                                                                                                                                                                                                                           Proteins AZ3021 encoded by clone AZ3021 from human adult colon, and BD12716 encoded by clone BD12716 from human fetal kidney cDNA library, useful for treating e.g. multiple sclerosis and rheumatoid arthritis.
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Best Local Similarity 90.7%; Pred. No. 5.7e-229;
Matches 794; Conservative 0; Mismatches 69; Indels 12;
                                                                                                                                Collins-Racie LA, Evans C;
Spaulding V, Carlin-Duckett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2946 BP; 858 A; 801 C; 570 G; 717 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents cDNA encoding a human secreted protein.
                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 134; 412pp; English
                                                                                                                                  Lavallie ER,
                                                                                                                                                      Bowman MR,
                 97US-00867677.
97US-00924838.
99US-00413232.
                                                                                                (GEMY ) GENETICS INST INC.
                                                                                                                                                      Treacy M,
                                                                                                                                Jacobs K, Mccoy JM,
Merberg D, Treacy M,
Kelleher K;
                                                                                                                                                                                                                 WPI; 2003-657236/62.
                                                                                                                                                                                                                               P-PSDB; ADC38777.
                     02-JUN-1997;
05-SEP-1997;
06-OCT-1999;
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The present sequence encodes a human endogenous retrovirus envelope protein. The specification describes a method for detecting expression of an envelope protein from a human endogenous retrovirus (HERV), in cells, of a tissue or culture. The method comprises detecting syncytia formation due to the fusogenic properties of the envelope protein. Envelope polypoptides and polynucleotides are used to produce therapeutic or prophylactic compositions, particularly for treatment of cancer, to correct defects in placental development (or other natural formation of other types of syncytia), and to promote adhesion of cells in grafts or cellular repair processes. Expression of sequences antisense to the polynucleotide are used to prevent formation of syncytia
2777 AATCATCTATTGCCTGAGAGCACAGGAGGAGAAATGATCGGGATATAAACCCAAGTC 2836
                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of a human endogenous retrovirus envelope protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTT
                                                                      tricgadecedebacedebaceceerrredgreeceerecerretaredgadereretrir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting expression of human endogenous retrovirus envelope prote cells of a tissue or culture, from its ability to induce syncytia.
                                                                                                                                                                                                                                                                                                                                                                                 Envelope protein; HERV; syncytia formation; placental development;
syncytia; cancer; cell adhesion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.9%; Score 730.2; DB 5; Length 2781; llarity 90.6%; Pred. No. 1.8e-228; Conservative 0; Mismatches 70; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2781 BP; 747 A; 770 C; 556 G; 708 T; 0 U; 0 Other;
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                                                                                                                                CATGCTATTTCACTCTATTAAATCTTGCAACTGC 2930
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/product= "envelope protein"
                                                                                                             CACTCTATTTCACTCTATTAAATCATGCAACTGC
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(INRM ) INST NAT SANTE & RECH MEDICALE.
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762. .2378
                          TTCAAGCCAGCAACAGCAACCCCT
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99FR-00011793
                                                                                                                                                                                                                                         AAF55630 standard; DNA; 2781
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human endogenous retrovirus.
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P-PSDB; AAB67652.
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Best Local Similarity
Matches 793; Conserv
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15-SEP-1999;
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                                                                                                             The invention relates to identifying compounds which are modulators of syncytin expression. The syncytin modulators are useful in diagnosis and treatment of preeclampala and gestational trophoblast disorders (e.g. choriocarcinoma, hydatiform mole, placental site tumour and missed/incomplete abortion). Syncytin is a human gene derived from the envelope gene of human endogenous defective retrovirus, HRRV-W. The present invention is based partly on the discovery that syncytin expression is dramatically reduced in preeclampaia, and is also mis-localised to the apical syncytiotrophoblast membrane. The present sequence is human
         developing preeclampsia, comprises determining whether the expression or activity of syncytin in the cell is modulated in the presence of a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cgaagcrgraaaacra-----caaarggagcccaagargcagrccaagacraa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2417 GATCTACCGCAGACCCTGGACCGGCCTGCTAGCCCACGATCTGATGATGACATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG
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                                                                                                                                                                                                                                                                                                                                                         Length 2930;
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                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                       Score 730.8; DB 6;
Pred. No. 1.2e-228;
0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                 Disclosure, Page 39-42; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.7%;
Matches 793; Conservative
                                                                                                                                                                                                                                                                                    syncytin cDNA
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31-MAR-2000; 2000US-00540217.
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                                               30-MAR-2001; 2001WO-US008631
                                                                                                                                           2001-639362/73
                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                     P-PSDB; ABG20023
         WO200175067-A2
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                             11-OCT-2001
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                                                                          CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTCTTAGGACCTCTAGCAGCTATAATATT
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                     AGGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGA
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromesome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consists of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cupplement. (II) and its binding partners are useful in medical imaging cupplypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful in medical imaging consolution polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format, incoming acid. 1415 GCTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTTTCCAGAAT 1474 1294 1354 ccrcasccaarssarsccrissarrcrcccrrrrassaccrcrascascraraararr 1414 16; 123 180 240 300 120 TGAAGCTGTAAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA 360 9 1175 TCAAAATCGAAGAGCTTTAGACCTTCTAACCGCTGAAAGAGGGGGAACCTGTTTATTTT AGGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAAAGTTAAAGA 1235 AGGGGAAGAATGCTGTTATTATGTTAATCAATCCGGAATCGTCACTGAGAAAGTTAAAGA AATTTGAGATCGAATATAATGTAGAGCAGAGGACCTTCAAAACACTGCACCCTGGGGGCCT CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTTAGGACCTCTAGCAGCTATAATATT TITACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTTCCAGAAT Gaps TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity. 74; Sequence 6394 BP; 1840 A; 1597 C; 1384 G; 1571 T; 0 U; 2 Other; Length 6394; Indels Score 728.6; DB 5; Pred. No. 1e-227; 0; Mismatches 223; Claim 1; SEQ ID NO 20014; 103pp; English ftp.wipo.int/pub/published\_pct\_sequences ; 0 54.8**%**; 78.6**%**; Query Match
Best Local Similarity 78.6
Matches 1094; Conservative 1295 1355 241 301 61 121 181 à g g ò g ò ò

> Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss. novel human diagnostic protein #20014.

6394

AAS84210 standard; cDNA;

RESULT 20

(first entry)

13-FEB-2002

AAS84210;

DNA encoding

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Homo sapiens

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This sequence represents the complete sequence of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulin- dependent diabetes and related pathologies) and of abnormal or susceptibility to these conditions, or proximity markers for associated with this susceptibility
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                                                                                                                                                                                Clone; human endogenous retrovirus; genome; autoimmune disease; multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diabetes; disseminated lupus erythematosus; pregnancy; chromosomal marker; ss.
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88.5%; Pred. No. 1.16
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Matches 774; Conservative
2543 CCCCGGTAACA 2553
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Autoimmune disease; retrovirus; human endogenous retrovirus W; HERV-W; gag gene; pregnancy; multiple sclerosis; T cell proliferation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents an endogenetic retrovirus, which is associated with an autoimmune disease, and is integrated into the human genome. The retrovirus is human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. HERV-W nucleic acid fragments, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor I cell proliferation in vitro
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88.5%; Pred. No. 1.1e-225;
ative 19; Mismatches 70;
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(HERV) W genome. The nucleic acids, their fragments or peptides enco by them are markers of autoimmune disease (e.g. multiple aclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulindependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes associated with this susceptibility
                                                                                                                                                12;
                                                                                                                      Length 1136;
                                                                                               Sequence 1136 BP; 336 A; 289 C; 241 G; 270 T; 0 U; 0 Other;
                                                                                                                                                Indels
                                                                                                                     Score 721.2; DB 2;
Pred. No. 9.9e-226;
0; Mismatches 75;
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                                                                                                               AAGCAGTTAGAGCGGTSGTCGGCCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
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                                      AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG
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Clone; human endogenous retrovirus; genome; autoimmune disease; multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diabetes; disseminated lupus erythematosus; pregnancy; chromosomal marker; ss.
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494 GCTACTCCTTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTTTCCAGAAT
                                                                                                361 AATCTACCGTGGACCCCTGGCCTGCTAGACTATGCTCTGATGTTAATGACATTGA
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                                                                                                                                                                                                                                                                                          541 GGGTGGACTGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATTCGAGATCGAATACAACGTAGAGCAGAAGACTTCGAAACACTGGACCTTGGGCCT
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                                                                                                                                                                       gene and 3' non coding sequences of HERV-W from human genome
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Best Local Similarity 90.0%; Pred. No. 9.9e-226;
Matches 787; Conservative 0; Mismatches 75;
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New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy.
                                                              This sequence represents clone cl.PH74 of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulinteumatoid dispetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes
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L.1e-222;
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                                                                                                                                                                                   Score 712.6; E
Pred. No. 1.1e-
0; Mismatches
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                                             Claim 1; Page 60-63; 106pp; French
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The present sequence represents an endogenetic retroviral nucleic acid fragment, which is associated with an autoimmune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HERV-W;
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TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT
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                                                                                                                                                                                                                                                                                                                                            Human endogenous retrovirus; HERV-W; HERV; chromosome 7; env protein; envelope protein; multiple sclerosis-related superantigen; vaccine; surface antigen; transmembrane; multiple sclerosis; neuroprotective;
                                       241 TTTACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT
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On the basis of the PBS t-RNA motif used for the classification of human changenous retrovirus (HERV9) the full length endogenous provirus which endogenous retrovirus (HERV9) the full length endogenous provirus which was been located on the long arm of human chromosome 7 (7021-22) has been certificated HERV-W. The present invention describes proteins or peptides (I) having superantigen (SA9) activity comprising the ENV protein (ENV) of HERV-W, the surface protein (SU) and transmembrane (TW) sub-units. (I) have neuroprotective activity, and can be used in: vaccines; antisense-therapy; and HERV-W SA9 activity-inhibitors. (I) and encoding DNA/RNA are useful for diagnosing multiple sclerosis (MS) or HERV-W-associated disorders. (I) are also useful for identifying substances and optionally crowering) capable of binding to a retroviral superantigen associated with MS, substances capable of blocking transcription or translation of HERV-W retroviral superanting an immune response capable of blocking transcription or translation of HERV-W retroviral SA9 is useful in therapy. Nucleic act adding to a retroviral capable of blocking sA9 activity, appable of blocking transcription or capable of blocking transcription or capable of blocking sA9 activity. Appable of blocking transcription or translation of HERV-W retroviral superantigen for use in treating or preventing MS, obtained using (I) are useful for the treatment and prevention of MS. (I) and nucleic acids encoding them are useful for another the present encodes the
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Pred. No. 1.1e-222;
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AGAGGAAAATGCTGTTGTTATGTTAATCAGTCGGAATCATCACCGAGAAAGTTAAAGA 1080
                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                              The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          961 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCGGGAAAGCGGGGAACCTTTTTATTTTT
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00668408.
03-AUG-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
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gene expression in human fetal liver.
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                                                                                                                                                                                                  ANCTEGGAAGGTGACCGCATCCATCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCG
                                                                           ACCAATC-----AGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAA
                                                                                                                                                                                                                                                                                                                                                          GCAATAGCCAATCATTGCCTGAGAGCACAGGGGGAAGGACAAGGATTGGGATATAA
                  AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTTCCTGTTGAGA
AATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGATGACATTGA
                                                            AGICACCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG
                                                                                                                                                                            GGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human breast cell single exon nucleic acid probe #4517
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26-MAY-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATTCAAGGTCGAATATAACGTAGCAAAGGAGCTGCAAAACACTGGACCCTGGGGCCT
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                                                                                placenta
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                                                                                                          Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder; ss.
                                                                              used to measure gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 4666; 654pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression in human placenta.
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26-MAY-2000; 2000US-0207456P.
30-UNY-2000; 2000US-0608408.
03-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
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                                                     (first entry)
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Matches 770, Conservative
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GAAATAGCCAATCATCTGTTGCCTGACAGCACCAGGAGGACAATGATCGGGATATAA 1740
                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                      772 ACTCAGGCATTCAAGCCAGCAACCGCACTTGGGTCCCCTCCCATGTATGGAGAG
                                                                                                                                           GCAATAGCCAATCATCTATTGCCTGAGAGCACAGCGGAAAGGACAAGGATTGGGATATAA
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
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                                                                                                                                              The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the reach of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring the invention presents a far greater diversity of probes for measuring microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this part did not form part of the printed specification, but was obtained the invention of the invention of the invention approach.
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for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
                                                                                        Claim 1; SEQ ID NO 4517; 327pp + Sequence Listing; English.
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89.7%; Pred. No. 3.3e-220;
ive 0; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                770; Conservative
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow asmples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
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                    marrow expressed exon; gene expression analysis; probe; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                   genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
marrow expressed single exon probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 4575; 658pp + Sequence Listing;
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Pred. No. 3.3e-220;
0; Mismatches 79;
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                                                                                                                                                                                                                                                                                                                                gene expression in human bone marrow.
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2000US-0207456P.
2000US-00608408.
2000US-0053468.
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89.7%;
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                        Human; bone marrow
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26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
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89.7%;
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1441 AAGCAGTTAGAGTGGTTGTTGGCCAACCTCCCCAACAGCAGTTGGGGTTTTCCTGTTGAGA 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
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                                                                                                                                                                                                                                                                                                                                                                               Human; single exon nucleic acid probe; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease; ss.
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Pred. No. 3.3e-220;
); Mismatches 79;
                                                                                                                                                                                                                                                                                                                                  Human liver single exon probe, SEQ ID No 4660.
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2000US-0234687P.
2000US-0236359P.
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2000US-0207456P.
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llarity 89.7%;
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tes 770; Conserv
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27-SEP-2000;
04-OCT-2000;
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                                                                                      601 ANCIGGGAAGGIGACCGCAICCAICTITAAACAIGGGGCTIGCAACTIAGCTCACACCCG
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                                                                                                                                                                                                                                                                661 ACCAATC-----AGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAA
                                                        GGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT
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; 2000US-020445B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and noncarding tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                       measuring gene expression in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                          Novel single exon nucleic acid probe used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 4413; 322pp; English
                                                                                                                                                                                                                                                                                                   Rank DR
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                                                                                                                                                                                                                                                                                                      Chen W,
                                                                                                                 2000US-00632366.
2000US-0234687P.
2000US-0236359P.
                                                                   2000US-0207456P
2000US-00608408
                                                                                                                 03-AUG-2000; 2000US-00632366
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                   26-MAY-2000;
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12819 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes of the human lung, manaling at high stringency to a nucleic conflection of detectably labeled nucleic acids derived from human lung manaly, and (b) measuring the label detectably bound to each probe of the array, identifying exons in a eukaryotic genome, comprising (a) and principly prodicting at least one exon from genomic sequences of the enkaryote; and (b) detecting specific hybridisation of detectably and (b) measuring the label detectably bound to each probe of the enkaryote; and (b) detecting specific hybridisation of detectably a rangorithmically prodicting at least one exon from genomic sequences of the enkaryote; and (b) detecting specific hybridisation of detectably having a fragment identical to the predicted exon, the probe is included comprising (a) measuring the expression of each of the exons in several comprising (a) measuring the expression of each of the exons in several comprising (a) measuring the expression of each of the exons in several microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single gene; a peptide comprising one of the exons in the tissues and/or cell types using ptyx diseases such as such an alygis, and for identifying exons in a gene; particularly using human companies, or the exons should be assigned to a single gene; a peptide comprising or analygis, and for identifying exons in a gene; particularly using human companies, pulmonary hamanes, particularly using human companies, pulmonary hamanes, pulmonary particularly using human pattern squence farmed for this patent did not form part of the print of the exo specification, but was obtained in electron: at ftp.wipo.int/pub/published\_pct\_sequences 

ä Gaps ., , Length 1894; Sequence 1894 BP; 557 A; 500 C; 361 G; 476 T; 0 U; 0 Other; Indels 53.0%; Score 704.8; DB 6; 89.7%; Pred. No. 3.3e-220; ive 0; Mismatches 79; Best Local Similarity 89.7 Matches 770; Conservative Query Match

9

1 TCAAAATCGAAGAGCTTTAGACTTGCTAAACCGCCAAAAGAGGGGGGAACCTGTTTATTTT

1140 1200 1260 1320 1020 1080 300 360 240 120 180 AATCIACCGIGGACCCCIGGACCGGCCTGCTAGACTAIGCTCTGAIGITAAIGACAITGA 420 AGAGGAAAAATGCTGTTATGTTAATCAATCCGGAATCATCACGAGAAAGTTAAAGA 1081 aarrcaaggregaararargragagcaaaggagcregaaacaraggacceg CCTCAGCCAATGGATGCCCTGGACTCCCCCTTCTTAGGACCTCTAGCAGCTATAATATT 1141 CCTCAGCCAATGGATGCCCTGGATTCTCCCCCTTCTAGGACCTCTAGCAGCTATAATATT TITACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTTTCCAGAAT GTTACTCCTCTTTGGACCCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTTTTCCAGAAT TGAAGCTGTAAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA AGGGGAAGAATGCTGTTAATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAAGA AATTTGAGATCGAATATATGTAGAGCAGAGGACCTTCAAAACACTGCACCCTGGGGCCT 61 1021 1201 301 1261 1321 961 121 181 241 361 셤 ઠે 요 ઠે ద ઠે ద ò g ò 셤 ò ò

1680 1740 1501 GGGGGGACTGAGAGAGAGAATAACTAGATTTCCTAGACCAACTAAGAATCCCTAAGACT 1560 540 9 771 1561 AGCTGGGAAGGTGACCGCTTCCACCTTAAACACCGGGCTTGCAACTTAGCTCACGCCCA 1681 GAAATAGCCAATCATCTGTTGCCTGACAGCACACCAGGAGGACAATGATGATCGGGGATATAA ANCTIGGGAAGGTGACCGCATCCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCG GCAATAGCCAATCATCTATTGCCTGAGAGCACAGCGGGAAGGACAAGGATTGGGATATAA 1441 AAGCAGTTAGAGTGGTTGTTGGCCAACCTCCCCAACAGCAGTTGGGTTTTTCCTTGAGA 541 GGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT ACCAATC-----AGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAA AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG 1801 Crcrcrrcrcrcrarr 1818 CTCTGTTTTCACTCTATT 849 601 661 712 832 481 421 RESULT 38 AAS77313

Human, chromosome mapping, gene mapping; gene therapy, forensic; food supplement, medical imaging, diagnostic; genetic disorder; ss. DNA encoding novel human diagnostic protein #13117. AAS77313 standard; cDNA; 2942 BP (first entry) WO200175067-A2 Homo sapiens. 13-FEB-2002 11-OCT-2001. AAS77313; 

YT; 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. 30-MAR-2001; 2001WO-US008631 Tang Drmanac RT, Liu C, (HYSE-) HYSEQ INC.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess WPI; 2001-639362/73. P-PSDB; ABG13126. biodiversity

Claim 1; SEQ ID NO 13117; 103pp; English

The invention relates to isolated polynucleotide (I) and polypeptide (II)

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sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed carbon (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food polypeptide in tissue, as molecular weight markers and as a food of stess expressing (II). (I) and its binding partners are useful in medical imaging of stess expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodivarity responsible for genetic disorders or other traits to assess biodivarity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this electronic format directly from WIPO at the private of product format directly from WIPO at the private of products dependent on DNA and electronic format directly from WIPO at
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Pred. No. 4e-212;
0; Mismatches 127; Indels
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Best Local Similarity 83.1%;
Matches 863; Conservative (
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   1982 IGTCACAGACCCACAGCTGACTTCCATCCCTCTG-
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23-AUG-2000; 2000US-00649167.
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The present invention relates to new nucleic acid sequences of human endogenouse retrovirus, HERV-7q, which is located on chromosome 7q. Regulatory elements associated with HERV-7q may alter expression of other genes (even remote genes) on the same chromosome, inducing immunological and/or neurological changes (which may be pathological or protective/curative). HERV-7q peptides can be used to improve efficiency of the immunotherapy. HERV-7q peptides and their coding sequences can be used in immunogenic or vaccinating compositions, for protection against autoimmune diseases, particularly multiple sclerosis. The peptides may also be used (by sequence comparison) to detect/identify endogenous retroviruses that are abnormally expressed in cancer, neuropathologies or other autoimmune diseases. The present sequence was 841 New nucleic acid sequences of human endogenous retrovirus, HERV-7q, use for diagnosis, treatment and prevention of autoimmune and neurological ATCTGGAATCATTACTGAGAAAGTTAAAGAAATTTGAGATCGAATATAATGTAGAGCAGA TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTT ----TATGTTAATCA Gaps Sequence 46340 BP; 16104 A; 8738 C; 8434 G; 13064 T; 0 U; 0 Other; Length 46340; 46; AATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGTATC Autoimmune disease; HERV-7q; chromosome 7q; immunotherapy; Indels 88; DB 3; Score 643.4; DB 3; Pred. No. 3.6e-199; RECH MEDICALE. 0; Mismatches Claim 15; Page 186-199; 225pp; French. AGGGGAAGAATGCTGTTAG---to illustrate the invention BP. SANTE & ABN97978 standard; DNA; 46340 Rieger 48.4%; 99WO-FR001513 98FR-00007920 Human endogenous retrovirus. 01-AUG-2002 (first entry) seguence Query Match
Best Local Similarity 85.4
Matches 781; Conservative (INRM ) INSERM INST NAT Perin J, WPI; 2000-160587/14. multiple sclerosis; Human retroviral 23-JUN-1999; 23-JUN-1998; WO9967395-A1 29-DEC-1999. Alliel PM, 842 61 91 1152 ABN97978; diseases. used RESULT 40 ABN97978 g., 8 ద ద 유 ò 1092 TAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTCTTCCATGACCCACGGCTTCT 1151

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Sequence 15019, A
Sequence 13633, A
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Sequence 17382, A
Sequence 3, Appli
                                                                                                                                                                           February 21, 2005, 06:54:34; Search time 234.166 Seconds (without alignments) 9286.612 Million cell updates/sec
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Query Match         99.8%;         Score 1326;         DB 4;         Length 1329;           Best Local Similarity 100.0%;         Pred. No. 0;         0;         Indels 0;         0;           Astches 1329;         Conservative 0;         Mismatches 0;         Indels 0;         0;           Qy         1 TCAAAATCGAAGGCTTTAGACTGCTAACGGCCAAAGAGGGGGAACTGTTTATTTT 60         0           Qy         61 AGGGAAGAATGCTTTAGACTTGCTAACGCCCAAAGAGGGGGAACTGTTATTTTT 60           Db         61 AGGGAAGAATGCTTTAGTTAATCAATCTGGAATCATTACTGAGAAGTTAAAGA 120           Db         121 AATTTGAGATGGTTAATGATGTTAATCAATCTGGAATCATTACTGAGAAGTTAAAGA 120           Db         121 AATTTGAGATGGATGTTAATGAGGGACCTTCAAAACACTGCACCTGGGGCT 180           Qy         121 AATTTGAGATGAATATAATGAGAGGACCTTCCAAAACACTGCACCTGGGGCT 180           Db         121 AATTTGAGATGCCTGGACTCTCCCCTTCTTAGGACCTTCTAAGACTATAATATT 240           Db         181 CCTCACCAATGGATGCCTGGACTCTCCCTTCTTAAGACTTCTTAAGACTTTTATATATT 240           CTCAGCCAATGGATGCCTGGACTCTCCACTTCTTAAGACTTGCTGATAATATT 240           Db         181 TTTACTCCTCTTTGGACCCTGCATCTTCAAAACTTGCTGATAATATT 240           CATTAACTCCTCTTTGGACCTTCTAAAACTTGCTGATAATATTGTCTCTTCCAGAAT 300           CATTAACTCCTCTTTGGACCTTCTTAAGATTGTTTTTAAGTTTGTCTTTCCAGAAT 300           CATTAACTCCTCTTTGGACCTTCTTAAGACTTGTTAAGATTGTCTTTCCAGAAT 300	301 301 361 361 421 481 601 601	

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APPLICANT: LaVallie, Edward R.
APPLICANT: COllins Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Mr. Sha
APPLICANT: M. Sha
APPLICANT: M. Sha
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6006B.AJ172A
CURRENT FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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CORGANISM: Homo sapiens
US-09-175-928-3
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Sequence 3, Application US/09175928A Patent No. 6312921 GENERAL INFORMATION: APPLICANT: Jacobs, Kenneth APPLICANT: McCOy, John M.

US-09-175-928-3

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Sequence 13002/C
; Sequence 13002/C
; Sequence 13002, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, V. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    PRIOR APPLICATION NUMBER: US/09/949,016
    PRIOR APPLICATION NUMBER: 60/231,768
    PRIOR PILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-09-08
    NUMBER OF SEQ ID NOS: 207012
    SOC ID NO 13002
    LENTH: 168394
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Pred. No. 2.3e-237;
0; Mismatches 134;
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| LOCATION: (1)...(168394)

| OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13002
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Best Local Similarity
Matches 878; Conserval
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASESEQ For Windows Version 4.0
SEQ ID NO 5640
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           2775 AATCATCTATTGCCTGAGAGCACAGGAGGAGAAATGATCGGGATATAAACCCAAGTC 2834
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                                                                                                                                           CATGCTATTTCACTCTATTAAATCTTGCAACTGCA 2929
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Pred. No. 6.8e-239;
0; Mismatches 70;
                                                                                                                      CACTCTATTTCACTCTATTAATCATGCAACTGCA 875
                                                                                                                                                                                                                                           Sequence 5640, Application US/09949016
Patent No. 6812339
                                                    TTCAAGCCAGCAACAGCAACCCCCTT
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Best Local Similarity 90.6%;
Matches 792; Conservative
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ORGANISM: Human
                                                                                                                                                                                                                   RESULT 4
US-09-949-016-5640
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                                                                                                                                                                                                                         Query Match
49.3%; Score 654.8; DB 4;
Best Local Similarity 83.5%; Pred. No. 2.5e-212;
Matches 844; Conservative 0; Mismatches 140;
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for windows Version 4.;
LENGTH: 77772
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                                                                                                                                                                       ; LOCATION: (1)...(77772)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-17417
                                                                                                                                                             NAME/KEY: misc_feature
                                                                                                                     TYPE: DNA
ORGANISM: Human
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                     TATTGCCTGAGAGCACAGGGAAGGACAAGGATTGGGATATAAACTCAGGCATTCAAGC
                                                         497 TGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTTCCTGTTGAGAGGGTGGACTGAGAGAG
                                                                                                          AGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGGGAAGGTGACC
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER,
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND IFILE REPERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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US-09-949-016-15858/C

JGENERAL INCOFFACTION US/09949016

GENERAL INCOFFACTION

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15558
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                                     AGCCAGCAACAACCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTCACT
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                                                                                                       -AGAGAGCTCACTAAAATGCTAATCAGGC-AAAAACAGGAGGTAAAGCAATAGCCA-ATC
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Pred. No. 3.2e-208;
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Best Local Similarity
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; ORGANISM: Human
US-09-949-016-15858
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; Sequence 12249, Application US/09949016
; Patent No. 6912339
; GENERAL INFORMATION:
    APPLICANT: VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, VENTER, V
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257 CCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTTTCCAGAATTGAAGCTGTAAAGCTA
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49.3%; Score 654.8; DB 4;
Best Local Similarity 83.5%; Pred. No. 2.5e-212;
Matches 844; Conservative 0; Mismatches 140;
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; LOCATION: (1)...(77997)
GOTHER INFORMATION: n = A,T,C or G
US-09-949-016-12249
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US-09-949-016-12249/c
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         METHOD
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CANT: ROGAN, PETER
OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES
SEFERENCE: 30307
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NAME/KEY: rerpeat region
LOCATION: (1). (780)
OTHER INFORMATION: ltr17
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
TITLE: Prototypic sequences for human repetitive DNA
JOURNE: 35
ISSUE: 4
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7.8e-208;
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90.0%; Pred. No. e.c.
... 0; Mismatches
            TITLE OF INVENTION: SINGLE COPY GENOMIC FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT FILED DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 479
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                       711; Conservative
                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            , DATABASE ENTRY
US-09-573-080A-385
                                                                                           SEQ ID NO 385
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     88; Indels
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Sequence 385, Application US/09573080A Patent No. 6828097 GENERAL INFORMATION: APPLICANT: JOAN, KNOLL

US-09-573-080A-385

141918

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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PAPLICATION NUMBER: 60/241,755
PRIOR PAPLICATION NUMBER: 60/241,768
PRIOR PAPLICATION NUMBER: 60/231,498
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15086
LENGTH: 219964
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                                  142096 AGCTGAAGTTTCGCTCG-CGTCCACTGCTGTTTGCCGCTGTCACAGACCTGCCGCTG
                                                                                                           ATTGCCTGAGAGCACAGGGGAAGGACAAGATTGGGATATAAACTCAGGCATTCAAGCC
                                                                                     ACTICCATCCCTTIGGAICCAGCAGAGTGICCACTGIGCICCTGAICCAGCGAGGIACCC
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43.8%; Score 582; DB 4; I
Best Local Similarity 87.3%; Pred. No. 5.2e-187;
Matches 687; Conservative 0; Mismatches 83;
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; ORGANISM: Human
US-09-949-016-15086
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Patent No. 6812339

GENERAL INFORMATION:
PAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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                CCCACGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGA
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llarity 89.3%; Pred. No. 4.8e-205;
Conservative 0; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15497
LENGTH: 245286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(245286)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-15497
                                                                                                                                                                                                                                 CCCAGTAACA 1329
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LOCATION: (1)...(24528
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693; Conserv
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US-09-949-016-15497/c
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Best Local Similarity 86.5
Matches 688; Conservative
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| GENERAL INFORMATION:
| GENERAL INFORMATION:
| JAPPLICANT: VENTER, J. Craig et al.
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF:
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF:
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF:
| CURRENT FILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SEQ ID NO 17420
| LEASESEQ FOR WINDOWS VERSION 4.0
| LEASESEQ FOR WINDOWS VERSION 4.0
| LEASESEQ FOR WINDOWS VERSION 4.0
| LEASESEQ FOR WINDOWS VERSION 4.0
| LEASESEQ FOR WINDOWS VERSION 4.0
| LEASESEQ FOR WINDOWS VERSION 4.0
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                                                                              TTCACTCTATTAAATCATGCAACTGCAC - TCTTCTGGTCCGTGTTTTTTATGGCTCAAG
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Patent No. 6812339
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LOCATION: (1)...(84571)
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OTHER INFORMATION: n =
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ORGANISM: Human
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RESULT 13
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Sequence 15393, Application US/09949016
Sequence 15393, Application US/09949016
Sequence 15393, Application US/09949016
Setent No. 6812339
Setent No. 6812339
Septicant: VENTER, J. Craig et al.
TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT PREIGNOWNER: US/09/949,016
CURRENT PRILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
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                                                                  ACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAA-GAATCCCNAAGCCTANCTG
                     Gaps
                       25;
                       Indels
Pred. No. 1.1e-181;
); Mismatches 82;
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99199 GGCCGGCCCATCTTGGGAGTGGCCAC 99225
                                                                                   ; Sequence 102, Application US/08979847B ; Patent No. 6582703 ; GENERAL INFORMATION:
                                                                                                                                                BESEME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, G
KOMURIAN-PRADEL, FL
JOLIVET-REYNAUD, CO
                                                                                                                                                                                                                     MANDRAND, BERNARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 635 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                              APPLICANT: PERRON, HERVE
BESEME, FREDERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 102:
                                                                                                                                                                                                                                     GARSON, JEREMY
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92.4%;
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Best Local Similarity 92.4
Matches 572; Conservative
                                                                          US-08-979-847B-102
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                                                                                                                                                                                Length 194790;
                                                                                                                                                                             42.3%; Score 562; DB 4; Length 19
82.8%; Pred. No. 3.5e-180;
.ive 0; Mismatches 128; Indels
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    PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FABLSEQ for Windows Version 4.0
SEQ ID NO 15393
                                                                                                                                                                                               Best Local Similarity 82.8
Matches 718; Conservative
                                                                                                                         TYPE: DNA
CRGANISM: Human
US-09-949-016-15393
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TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMBUTER: Talm PC Compatible

COMPUTER: Talm PC Compatible

COMPUTER: Talm PC Compatible

COMPUTER: DatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979 847B

FILING DATE: 26-No. 6582703-1997

CLASSIFICATION: «Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: 30,024

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 635,
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Pred. No. 4.3e-176;
0; Mismatches 47;
                                                        THERAPEUTIC PURPOSES
                                                                                 NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID NO: 102: US-08-979-847B-102
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JERICAL INFORMATION:

JAPPICANT: VENTEL, J. Craig et al.

APPLICANT: VENTEL, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FEASISEQ for Windows Version 4.0

LENGTH: 116652
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OTHER INFORMATION: n = A,T,C
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ORGANISM: Human
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; Sequence 17002, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFRENCE: CLOA01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FRESEQ for Windows Version 4.0
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| LOCATION: (1)...(140224)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17002
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Best Local Similarity 82.4
Matches 631; Conservative
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ORGANISM: Human
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US-09-949-016-17002
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US-09-949-016-11757/C
US-09-949-016-11757, Application US/09949016
Facuence 101757, Application US/09949016
Facuence 061239
GENERAL INFORMATION:
FAPPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION WUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
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Score 478.6; DB 4;
Pred. No. 1.1e-151;
0; Mismatches 102;
 36.0%;
82.2%;
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Pred. No. 3.1e-148;
0; Mismatches 102;
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-31.498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FaetSEQ for Windows Version 4.; SEQ ID NO 11757
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    OTHER INFORMATION: n = A,T,C or
    US-09-949-016-11757
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 645; Conservative
                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (1)...(13163
                                                                                                                                                                                                         ORGANISM: Human
FEATURE:
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sequence 17057, Application US/09949016

patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOL1307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                              GAAGTGGCCCACTGCCATTTTGGTAGCGGCCCACCACCATCTTGGGAGCTGTGGGAGCAA
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Pred. No. 2e-140;
0; Mismatches 118; Indels 22;
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Best Local Similarity 81.3%;
Matches 607; Conservative
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US-09-949-016-17057
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                                   Sequence 17068, Application US/09949016

Sequence 17068, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOOD.
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
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Pred. No. 7.2e-148;
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Best Local Similarity 81.2%;
Matches 639; Conservative
                             -09-949-016-17068/c
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; ORGANISM: Human
US-09-949-016-17068
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Sequence 11973, Application US/09949016
; Sequence 11973, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WIMBER: 60/241,755
; FILE REFERENCE: 2000-10-0-4-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PELING DATE: 2000-10-0-3
; PRIOR PELING DATE: 2000-10-0-3
; PRIOR PELING DATE: 2000-10-0-3
; PRIOR PELING DATE: 2000-10-0-3
; PRIOR PELING DATE: 2000-0-0-10-3
; PRIOR PELING DATE: 2000-0-0-3
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1973
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larity 82.4%; Pred. No. 5.3e-140;
Conservative 0; Mismatches 106;
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LOCATION: (1).\(\tilde{\text{.}}\) (251682)
OTHER INFORMATION: n = A,T,C or G
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PELING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOCTHARE: PSHESEQ for Windows Version 4.0
SEQ ID NO 17296
LENTH: 251672
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             92647 ACCCACCATTGACTTCCACCCCTCCAGATCTGGCAGGTATCCACTGCACTTCTGATCCA 92706
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Best Local Similarity 82.4%; Pred. No. 5.3e-140;
Matches 599; Conservative 0; Mismatches 106;
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## Sequence 1741, Application US/09949016
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## Sequence 1741, Application US/09949016
## Sequence 1741, Application Sequence 1741, Application Sequence 1741, Application Sequence 1741, Application Sequence 1741, Application Sequence 1741, Application WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVERTION WIMBER: US/09/949,016
## CURRENT APPLICATION NUMBER: US/09/949,016
## CURRENT APPLICATION NUMBER: 60/241,755
## PRIOR PILING DATE: 2000-10-0337,768
## PRIOR FILING DATE: 2000-10-0337,768
## PRIOR FILING DATE: 2000-10-0337,768
## PRIOR APPLICATION NUMBER: 60/231,498
## PRIOR APPLICATION NUMBER: 60/231,498
## PRIOR APPLICATION NUMBER: 60/231,498
## PRIOR FILING DATE: 2000-09-08
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                                                                                                                             of repetitive elements (repbase)
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Prototypic sequences for human repetitive DNA .: Journal of Molecular Evolution
                                                                                                                                                                                                                               Score 440.4; DB 4;
Pred. No. 2.2e-139;
0; Mismatches 46;
                     JOURNAL: Journal of Molecular Evolution VOLUME: 35 ISSUE: 18SUE: 198-291 DATE: 1992-10-DATABASE ACCESSION NUMBER: Database of DATABASE ENTRY DATE: DATABASE ENTRY DATE: DATABASE ENTRY DATE: DATABASE ENTRY DATE: 1996-01-26
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Best Local Similarity 89.4%;
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US-09-949-016-17411/c
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LOCATION: (1)..(8523)
OTHER INPORMATION: herv17
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic,
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APPLICANT: ACGAN, PETER
TITLE OF INVENTION: SINGLE COPY GENOMIC HYB
FILE REFERENCE: 30307
CURRENT APPLICATION NUMBER: US/09/573,080A
CURRENT APPLICATION NUMBER: US/09/573,080A
NUMBER OF SEQ ID NOS: 479
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 8523
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US-09-573-080A-21
Sequence 21, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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SQUENCE 44299, Application US/09949016

Bequence 44299, Application US/09949016

Betent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

CURRENT FILING DATE: 2000-14-15

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                   15;
                                                                                                                                      Length 601;
                                                                                                                                                                   Indels
                                                                                                                                     Query Match 32.7%; Score 434.8; DB 4; Best Local Similarity 86.0%; Pred. No. 2.9e-138; Matches 520; Conservative 1; Mismatches 69;
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 202370
LENGTH: 601
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US-09-949-016-44299/c
                                                                            ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-202370
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: 08/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                             Gaps
                                                                                                                                                             12;
                                                                                                                            Length 99580;
                                                                                                                                                             Indels
                                                                                                                              DB 4;
                                                                                                                            Score 435.8; DB 4,
Pred. No. 4.7e-137,
0; Mismatches 74,
    NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17411
LENGTH: 99580
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; Sequence 202370, Application US/09949016
; Patent No. 6812339
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                                                                                                                                32.8%;
86.1%;
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                                                                                                                                                Similarity
                                                                                  ; ORGANISM: Human
US-09-949-016-17411
                                                                                                                                                              Matches 531;
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                                                                       TYPE: DNA ORGANISM:
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBERS: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15019
LENGTH: 57507
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'Sequence 13633, Application US/09949016

'Patent No. 681233

; GRMERAL INFORMATION:
                                                                                                                                    31.0%;
79.6%;
                                                                                                                                    Query Match
Best Local Similarity 79.6
Matches 592; Conservative
                                                                                                  , ORGANISM: Human
US-09-949-016-15019
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                                                                                      TYPE: DNA ORGANISM:
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Batent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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                                                                                                                           601;
                                                                                                                           Length
                                                                                                                                                  Indels
                                                                                                                         Score 427.8; DB 4;
Pred. No. 7.3e-136;
1; Mismatches 80;
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44299
LENGTH: 601
                                                                                                                          Query Match
Best Local Similarity 83.9%;
Matches 511; Conservative
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                                                                                        , ORGANISM: Human
US-09-949-016-44299
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57507;
     Length
                                                                                                             Indels
Score 411.4; DB 4;
Pred. No. 7.6e-129;
0; Mismatches 124;
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Sequence 11770, Application US/09949016
; Betent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REPERENCE: CLOOU1307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFFTMARE: PRESISEQ for Windows Version 4.0
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                                                                                     6051 AAAAAGGCTTGCCGCCATCTTGGGAGCCGCCTGCCCCATCTTGGG
                                                             1231 ANGTGAGGCTTGCCACCATTTGGGAAGTGGCCCACTGCCATTTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | NAME/KEY: misc_feature
| LOCATION: (1)...(49487)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11770
                                                                                                                                                               SULT 28
-09-949-016-11770/c
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LENGTH: 49487
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     APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307;
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ for Windows Verbion 4.0

SEQ ID NO 13633

LENGTH: 39686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 39686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 399.8; DB 4; Length
Pred. No. 5.7e-125;
0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(39686)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 30.1%;
Best Local Similarity 78.1%;
Matches 598; Conservative
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US-09-949-016-195793/C

1S-09-949-016-195793, Application US/09949016

1 Sequence 19579, Application US/09949016

1 Patent No. 6B12339

1 GENERAL INFORMATION:

1 TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 PRIOR APPLICATION NUMBER: 60/231,768

1 PRIOR PILING DATE: 2000-10-20

1 PRIOR PLING DATE: 2000-10-33

2 PRIOR FILING DATE: 2000-10-03

3 PRIOR FILING DATE: 2000-09-08

3 NUMBER OF SEQ ID NOS: 207012

4 SOCTIVE FEATSEQ for Windows Version 4.0

5 SEQ ID NO 195793

LENGTH: 601
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                                                                                                                                TATTGCCTGAGAGCACAGCGGGAAGGACAAGGATTGGGATATAAACTCAGGCATTCAAGC 787
                                                                                          136 AGAGAGTTCACTAAAATGCTAACTAGGGAAAAAAGAGGTAAAGAAATAGCCAATCATC 77
                                                                                                                                                    AAGCTGAGCTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACAGACCCGCTGCT
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                   668 AGAGAGCTCACTAAAATGCTAATCAGGC-AAAAACAGGAGGTAAAAGCAATAG-CCAATCA
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82.3%; Pred. No. 2...
1; Mismatches
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Matches 487; Conservative
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Sequence 44300, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TUTLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR PLILOR DATE: 2000-04-14

PRIOR PLILOR DATE: 2000-10-20

PRIOR PELICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLILOR DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: PRACESEQ for Windows Version 4.0

SEG ID NO 44300
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Pred. No. 5.4e-122;
1; Mismatches 64;
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Best Local Similarity 85.9%;
Matches 477; Conservative
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US-09-949-016-44300
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Sequence 146564, Application US/09949016

Fatent No. 6812339

GENERAL INFORMATION:

APPLICANT: VERNER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL0001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PLILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-010-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 146564
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406 TGAGCTGAACACTAGTCACGGTTCCACGGTTCTTCTGTGACCCGTGGCTTCTAATA
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Pred. No. 1.4e-107;
1; Mismatches 68
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Best Local Similarity 83.7%;
Matches 405; Conservative
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOJ307

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTIMARE: PESECRO for Windows Version 4.0

SEQ ID NO 44298

LENGTH: 601
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Pred. No. 7e-116;
1; Mismatches 76; Indels
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Patent No. 6812339
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Best Local Similarity 83.6°
Matches 432; Conservative
                                                                                                                                                                                                                                                                            RESULT 31
US-09-949-016-44298/C
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; ORGANISM: Human
US-09-949-016-44298
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Sequence 13590, Application US/09949016
Patent No. 6812339
GRNERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                            Sequence 21394, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59. US2.REC
CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 21394

LENGTH: 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.9%; Score 344.6; DB 4 Best Local Similarity 88.9%; Pred. No. 2.2e-107 Matches 394; Conservative 1; Mismatches 45
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US-09-513-999C-21394
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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LOCATION: 102
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US-09-949-016-13590/c
RESULT 33
US-09-513-999C-21394
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25.9%; Score 343.6; DB 4; Length 149971;
Best Local Similarity 79.7%; Pred. No. 2.9e-105;
Matches 488; Conservative 0; Mismatches 96; Indels 28;
           CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                 | NAME/KEY: misc_feature
| LCCATION: (1)...(149971)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13590
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                                                                                                                                                                                                         SEQ ID NO 13590
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; Sequence 133739, Application US/09949016

RESULT 35 US-09-949-016-133739/c

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Sequence 20257, Application US/09949016

Sequence 20257, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:
APPLICANTY VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: LC001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-20

PRIOR PELLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: FastSEQ for Windows Version 4.0

LENGTH: 601
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                                                                                                                                                                     Length 601;
                                                                                                                                                                        Score 336; DB 4; Length 60 Pred. No. 2.4e-104; 1; Mismatches 57; Indels
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; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 120277; LENGTH: 601.
; TYPE: DNA; ORGANISM: Human US-09-949-016-120277
                                                                                                                                                                     Query Match 25.3%;
Best Local Similarity 86.2%;
Matches 394; Conservative
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Sequence 120777, Application US/09949016
Sequence 120777, Application US/09949016
Sequence 120777, Application US/09949016
SEQUENCE 120777, Application US/09949016
SEQUENCE INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
STILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: 60/241,755
SPRIOR PILING DATE: 2000-10-20
SPRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-09-08
SPRIOR RILING DATE: 2000-09-08
SPRIOR RILING DATE: 2000-09-08
SPRIOR RILING DATE: 2000-09-08
SPRIOR RILING DATE: 2000-09-08
                           GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FaetSEQ for Windows Version 4.0
LENGTH: 601
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89.9%;
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Best Local Similarity 89.9
Matches 372; Conservative
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; ORGANISM: Human
US-09-949-016-133739
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Sequence 44297, Application US/09949016

Sequence 44297, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
Patent No. 10 Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOMINGT.
CURRENT FILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44297
LENGTH: 601
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23.9%; Score 317.6; DB 4; Length
Best Local Similarity 86.0%; Pred. No. 5e-98;
Matches 350; Conservative 1; Mismatches 56; Indels
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| Sequence 146565, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. | APPLICANT: VENTER, J. CRAIG et al. | TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED | TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF | FILE REFERENCE: CLOOL307 | CURRENT APPLICATION NUMBER: US/09/949,016 | CURRENT PILING DATE: 2000-04-14 | PRIOR APPLICATION NUMBER: 60/241,755 | PRIOR PILING DATE: 2000-10-20 | PRIOR FILING DATE: 2000-10-03 | PRIOR FILING DATE: 2000-10-03 | PRIOR FILING DATE: 2000-09-08 | NUMBER OF SEQ ID NOS: 207012 | SOFTWARE: FBSECSOF FOR WINDOWN VERSION 4.0 | SEQ ID NO 146565 | LENGTH: 601
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                      GCTACCCCCCCGTTGAATGGGAGCTCTGTTTTCACTCTATTAAATCTTGCAACTGCA---
                                                                869 AACTGCACTCTTCTGGTCCGTGTTTTTTATGGCTCAAGCTGAGCTTTTGTTCGCCATCCA
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Pred. No. 4.3e-98;
1; Mismatches 53;
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Best Local Similarity 85.2%;
Matches 369; Conservative
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US-09-949-016-146565
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US-09-949-016-146565
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US-09-949-016-44296/c

Sequence 44296, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOL1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSESEQ for Windows Version 4.0

SEG ID NO 44296
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292 CATGGCCCAAGATTCCATTCTTTGGAACCTTTGAGGCCAAGAACCCCAGGTCAGAGAACA 233
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                                        1234 TGAGGCTTGCCACCATTGGGAAGTGGCCCACTGCCATTTTGGTAGC 1280
                                                                    232 AGAGGCTTGCCGCTATCTTGGAAGGGGCCTGCCACCATCTTGGGAGC 186
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US-09-949-016-44296
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	.08, App	108, App	81, Appl	910, App	17, Appl	18, Appl	9936, Ap	4, Appli	Sequence 134, App	3, Appli	l, Appli
Description	Sequence 108, App										
ΩI	8 US-08-979-847-108	US-10-114-104-108	US-09-873-367C-81	US-10-087-192-910	US-10-220-120-17	US-10-637-565-18	US-10-198-846-9936	US-10-416-642-4	US-10-114-893-134	US-10-016-249-3	US-09-902-535-1
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% Query Match	9.66	99.8	77.9	60.1	58.6	58.3	58.3	57.7	55.1	55.1	55.0
Score	1326	1326	1035.2	798.2	778.8	775.4	774.2	766.8	731.8	731.8	730.8
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722.6 54.4 7582 1.71.2 54.3 1136 1.71.2 54.3 1136 1.71.2 54.3 1136 1.71.1 53.5 2.782 1.71.1 53.5 2.782 1.71.1 53.5 2.782 1.71.1 53.5 2.782 1.71.2 54.3 1.71.2 579.8 4.6 5.71.2 579.8 4.3 6.10.2 579.8 4.3 6.10.2 579.8 4.3 6.10.2 579.8 4.3 6.10.2 579.8 4.3 6.10.2 579.8 4.3 6.10.2 579.8 4.3 6.10.2 579.8 4.3 6.10.2 579.2 1.2 54.5 5.2 5.2 5.2 5.2 5.2 5.2 5.2 5.2 5.2 5	US-10-632-793-30			US-1	US-09-864-761-44									US-08-979-847-102	US-10-114-104-10	US-10-220-120-15	US-10-719-993-67	US-10-741-600-17	US-10-264-237-28	US-09-731-231A-3	US-10-751-985-3	US-10-719-993-70	US-10-741-600-17	8 US-10-719-993-6							US-10-027-632			1000 100 000 011
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## ALIGNMENTS

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RESULT 108
1 Sequence 108, Application US/08979847
5 Sequence 108, Application US/08979847
5 Sequence 108, Application US/08979847
5 PUBLICANT BERRON HERVE
APPLICANT BESEME, FREDERIC
APPLICANT BESING, FREDERIC
APPLICANT WANDRAND, EGRAND, COLETTE
APPLICANT TOULVET-REYNAUD, COLETTE
APPLICANT TOULVET-REYNAUD, COLETTE
APPLICANT TOULVET-REYNAUD, COLETTE
APPLICANT TOUR PARANHESE PROME APPLICANT TOUR PRENABL AND NUCLEOTIDE FRAGMENTS
1 TILLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLAC
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLAC
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, NUMBER OF SEQUENCES: 20
TITLE OF INVENTION: THERAPEUTIC PURPOSES
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
TITLE OF INVENTION SYSTEM: PC-DOS/MS-DOS
COMPUTER: INP PC COMPACTION DATA:
COMPUTER: PREABABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: PREABABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: PREABABLE FORM:
MEDIUM TYPE: PREABABLE FORM:
MEDIUM TYPE: PREABABLE FORM:
MEDIUM TYPE: PREABABLE FORM:
MEDIUM TYPE: PREABABLE FORM:
MEDIUM TYPE RELABILIATION NUMBER: US/08/979,847
FILLING DATE: 26-NOV-1997
CLARSENT APPLICATION: 435
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APPLICANT: FEBLE.
BESEME, FRED....
BESEME, FRED....
BESEME, FRED...
BESEME, FRED...
BESEME, FRED...
BESEME, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JERRHY
TUKE, PHILIP
TITLE OF INVENTION: VITAL MATERIAL AND NUCLEOTIDE FRAGMENTS
THERAPEUTIC PURPOSES
THERAPEUTIC PURPOSES
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                                                                                                                                               Version #1.30
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CORRESPONDENCE ADDRESS:
ADDRESSE: OLIFF & BERRIDGE, PLC
ADDRESSE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
COMPUTER: USA
ZIP: 22320
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vex
CURRENT APPLICATION DATE: US/10/114,104
FILING DATE: 03-APr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 108, Application US/10114104; Publication No. US20030198647A1
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99.8%; Score 1326; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1329; Conservative 0; Mismatches
        ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPAX: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 1329 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: STRANDEDNESS: Single
                                                                                                                                                                    MOLECULE TYPE: CDNA
                                                                                                                                                         linear
                                                                                                                                                                                US-08-979-847-108
                                                                                                                                                         TOPOLOGY:
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Sequence 81, Application US/09873367C

Sequence 81, Application US/09873367C

Publication No. US20030165839A1

GENERAL INFORMATION:

APPLICANT: Young, Paul

APPLICANT: Soppet. Daniel

APPLICANT: Bener, Reinhard

APPLICANT: Ener. Reinhard

APPLICANT: Ener. Reinhard

APPLICANT: Augustus, Meena

APPLICANT: Carter, Reinhard

APPLICANT: Carter, Reinhard

APPLICANT: Augustus, Meena

APPLICANT: Augustus, Meena

APPLICANT: Augustus, Meena

APPLICANT: Carter, Reinhard

APPLICANT: Augustus, Meena

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APPLICANT: Augustus, Meena

APPLICANT: Augustus, Meena

APPLICANT: Augustus, Meena

APPLICANT: Carter, Reinhard

APPLICANT: Augustus, Meena

APPLICANT: Augustus, Meena

APPLICANT: Augustus, Meena

APPLICANT: Soppet.

ITILE OF INVENTION: Signature Gene Sets

ITILE OF INVENTION: Signature Gene Sets

ITILE OF INVENTION: Signature Gene Sets

FILE REFERENCE: 689290-64

CURRENT APPLICATION NUMBER: U.S. 60/236,891

PRIOR PILING DATE: 2000-10-29

PRIOR FILING DATE: 2000-11-01

PRIOR FILING DATE: 2000-11-01

PRIOR FILING DATE: 2000-11-01

NUMBER OF SEQ ID NOS: 1067

SOFTWARE: Patentin version 3.0

SEQ ID NO 81

LENGTH: 56093
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             TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT
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100.0%; Pred. No. 0;
ive 0; Mismatches 0;
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,847
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-114-104-108
                                                                                                                            TELECOMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                       Query Match 99.8
Best Local Similarity 100.
Matches 1329; Conservative
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                                                         1021 ACCCATTGCCACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCC
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 910, Application US/10087192
; Sequence 910, Application US/10087192
; bublication No. US20020182586A1
; GENERAL INFORMATION:
    APPLICANT: Morris, David W.
    TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
    FILE REFERENCE: $29452000122
    CURRENT APPLICATION NUMBER: US/10/087,192
    CURRENT FILING DATE: 2002-03-01
    PRIOR PAPLICATION NUMBER: US 09/747,377
    PRIOR PLING DATE: 2000-12-22
    PRIOR PLING DATE: 2001-03-02
    PRIOR PLING DATE: 2001-03-02
    PRIOR FILING DATE: 2001-03-02
    NUMBER OF SEQ ID NOS: 2059
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | NAME/KEY: misc_feature
| LOCATION: (1)...(21646)
| OTHER INFORMATION: n = A,T,C or G
US-10-087-192-910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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US-10-087-192-910
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                                                                                                                                                      1 TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGGAACCTGTTTATTTT
                                                                                                                  Gaps
                                                                               DB 10; Length 56093;
                                                                                                                  13;
                                                                              Score 1035.2; DB 10; Lengt
Pred. No. 1.6e-310;
0; Mismatches 111; Indels
                                                                              Query Match
Best Local Similarity 90.1%;
Matches 1133; Conservative (
       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-81
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OTHER INFORMATION: Incyte ID No. US20040048253A1 LI:351965.1:2000FEB01
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Pred. No. 1.9e-231;
0; Mismatches 112; Indels
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; OTHER INFORMATION: a, t, c, g, or other
US-10-220-120-17
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                                                                                                                                                        STOCKDREHER, Theresa
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Best Local Similarity 87.2%;
Matches 904; Conservative
                                                                 LIU, Tommy F.
ROSEBERRY, Ann M.
ROSEN, Bruce H.
RUSSO, Frank D.
                                                                                                                                                                                DAFFO, Abel
WRIGHT, Rachel J.
YAP, Pierre E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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                                                                                                                                                                                                     .9991 ACTAMANTGCTAMTTAGGCAMAMACAGGAGGTAMAGAMATAGCCAMTCACCTTTTGCCTG 20050
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CIGCIGACITCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAG 1018
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                                                                                                                                                                                               Length 2030;
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                                                                                                                                                                                            Score 775.4; DB 17;
Pred. No. 2.7e-230;
0; Mismatches 63;
PRIOR APPLICATION NUMBER: EP 99420041.8
PRIOR FILING DATE: 1999-02-15
NUMBER OF SEQ ID NOS: 20
SCFTWARE: PatentIn version 3.0
SEQ ID NO 18
LENGTH: 2030
                                                                                                                                                                                              58.3%;
                                                                                       TYPE: DNA

ORGANISM: MSRV-1 retrovirus

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1626)

US-10-637-565-18
                                                                                                                                                                                                             Best Local Similarity 92.8
Matches 812; Conservative
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APPLICANT: PRAANHOS-BACCALA, Glaucia
APPLICANT: PERRON Herve
APPLICANT: WOUNTIAN-PRADEL, Florence
APPLICANT: WOUNTIAN-PRADEL, Florence
TITLE OF INVENTION: THE LITR REGION OF WSRV-1 AND THE PROTEINS IT ENCODES, AND PROBES
FILE REPERENCE: 110257
CURRENT BAPPLICATION NUMBER: US/10/637,565
CURRENT FLING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US/09/890,340
PRIOR APPLICATION NUMBER: PCT/IB00/00159
PRIOR FILING DATE: 2001-11-27
PRIOR FILING DATE: 2001-11-27
PRIOR FILING DATE: 2001-11-27
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Publication No. US20040043381A1
GENERAL INFORMATION:
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OTHER INFORMATION: Incyte ID No. US20040043452A1 7477736CB1
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Pred. No. 1.3e-227;
0; Mismatches 60; Indels
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; Sequence 4, Application US/10416642
; Publication No. US20040043452A1
; GENERAL INFORMATION:
; APPLICANT: NAWTUMAR, Jayalaxmi
; APPLICANT: RAWTUMAR, Jayalaxmi
; APPLICANT: RAWTUMAR, Jayalaxmi
; APPLICANT: PRAYZU, Chandra
; TITLE OF INVENTION: EMBRYGENESIS ASSOCIATED PROTEINS
; FILE REPERBURG: PF-0842 DT-071
; CURRENT APPLICATION NUMBER: US/10/416,642
; CURRENT FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: 60/249,407
; NUMBER OF SEQ 1D NOS: 4
; SOFTWARE: PERL PROGRAM
; SEQ 1D NO 4
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Best Local Similarity
Matches 812; Conserv
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US-10-416-642-4
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APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youthen
APPLICANT: Wang, Youthen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
FRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 7974
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0; Mismatches 126;
                          1980 CACTCTATTTCACTCTATTAAATCTTGCAACTGAA 2014
841 CACTCTATTTCACTCTATTAAATCATGCAACTGCA
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                                                                                                                                                                                                          Sequence 9936, Application US/10198846 Publication No. US20030099974A1 GENERAL INFORMATION:
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Best Local Similarity 95.8%;
Matches 937; Conservative (
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US-10-198-846-9936
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Publication No. US20020193567A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
APPLICANT: Werberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
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                                                                           THEM
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Kelleher, Kerry S.
TITLE OF INVENTION: SECRETE PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT APPLICATION NUMBER: 09/413,232
EARLIER FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 134
LENGTH: 2946
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Pred. No. 1.3e-216;
0; Mismatches 69;
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Best Local Similarity 90.7%;
Matches 794; Conservative C
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APPLICANT: Keith, Jr., James C.
APPLICANT: Mi, Sha
TITLE OF INVENTION: Methods and compositions for diagnosing
TITLE OF INVENTION: Methods and treating preeclampsia and gestational trophoblast
TITLE OF INVENTION: disorders
FILE REFERENCE: GIN-600681
CURRENT APPLICATION NUMBER: US/09/902,535
CURRENT APPLICATION NUMBER: 60/216,657
PRIOR APPLICATION NUMBER: 60/216,657
PRIOR PILING DATE: 2000-07-06
NUMBER OF SEQ 1D NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2129 AGGGGAAGATGCTGTTATTATGTTAATCATCCGGAATCGTCACTGAGAAAGTTAAAGA
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                    2535 AAGCAGTTAGAGCGGTCGTCGCCAACTCCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
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Pred. No. 2.7e-216;
0; Mismatches 69;
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Patent No. US20020102530A1
GENERAL INFORMATION:
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Best Local Similarity 90.7%;
Matches 793; Conservative (
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LOCATION: (930)...(2546)
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                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10016249
Fublication No. US20030100053A1
GENERAL INFORMATION
APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: Lavalide, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: McDery, David
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
APPLICANT: However a secretic by APPLICANT: APPLICANT: SECRETED PROFIEINS AND POLYNUCLEOTIDES ENCODING THEM
TILLE REFERENCE: 6006B.AJ172A
CURRENT APPLICATION NUMBER: US/09/175,928
FILCH PAPLICATION NUMBER: US/09/175,928
FRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 62
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                                                                                                          CACTCTATTTCACTCTATTAAATCATGCAACTGCA 875
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Pred. No. 1.3e-216;
0; Mismatches 69;
  TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCC
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Best Local Similarity 90.7%;
Matches 794; Conservative 0
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (2213).. (2213)
OTHER INFORMATION: n = a o:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2298).. (2398)
OTHER INFORMATION: n = a o:
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OTHER INFORMATION: n = a o:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4115)...(4115)
OTHER INFORMATION: n = a o:
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COCATION: (4261). (4261)

COTHER INFORMATION: n = a

US-10-632-793-30
                              LOCATION: (198]..(198)
OTHER INFORMATION: n = a
FEATURE:
NAME/KEY: misc feature
LOCATION: (307)..(307)
OTHER INFORMATION: n = a
FEATURE:
NAME/KEY: misc feature
LOCATION: (355)..(355)
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NAME/KEY: misc feature
LOCATION: (1331)..(1331)
OTHER INFORMATION: n = a
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LOCATION: (1309)...(1309)
OTHER INFORMATION: n = 8
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US-10-632-793-30
is Gequence 30, Application US/10632793
is Gequence 30, Application No. US20040048298A1
is GENERAL INFORMATION:
is APPLICANT: PARAMHOS-BACCALA, Glaucia
APPLICANT: PARAMHOS-BACCALA, Glaucia
APPLICANT: MALLET, Francois
TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
FILE REFERENCE: 110048
CURRENT APPLICATION NUMBER: US/10/632,793
CURRENT PILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 1999-01-21
PRIOR FILING DATE: 1999-01-21
PRIOR FILING DATE: 1999-01-21
PRIOR FILING DATE: 1999-01-21
SOFTWARE: PRECEIN VERSION 3.3
SOFTWARE: PRECEIN VERSION 3.3
LENGTH: 7582
TYPE: DNA
CURRENT: 7582
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TGAAGCTGTAAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA
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                                                            TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGGAACCTGTTTATTTT
                               12;
   DB 17; Length 7582;
                               Indels
                                70;
54.4%; Score 722.6; DB 17
88.5%; Pred. No. 1.6e-213;
tive 19; Mismatches 70;
 Query Match
Best Local Similarity 88.5%,
Matches 774; Conservative
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Sequence 26, Application US/10632793

Sequence 26, Application US/20040048298A1

GENERAL INFORMATION:
APPLICANT: PARANNOS-BACCALA, Glaucia
APPLICANT: PARANNOS-BACCALA, Glaucia
APPLICANT: MALLET, Francois
APPLICANT: WOISSET, Cecile
TITLE OF INVENTION: AUTOINMUNB DISEASE, LABELING METHOD AND REAGENT
TITLE OF INVENTION: AUTOINMUNB DISEASE, LABELING METHOD AND REAGENT
TITLE OF INVENTION: AUTOINMUNBER: US/10/632,793
CURRENT FILING DATE: 2003-08-04
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: PCT/FR00/00144
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: FR 99/00888
SPRIOR APPLICATION NUMBER: FR 99/00888
PRIOR APPLICATION NUMBER: FR 99/00888
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                                                           CCTCAGCCAATGGATGCCCTGGACTCTCCCCTTTAGGACCTCTAGCAGCTATAATATT
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             481 AAGCAGITAGAGCAGITGICAGCCAACCICCCCAACAGCACTIGGGIT
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US-10-632-793-26
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Sequence 25, Application US/10632793

Publication No. US20040048298A1

GENERAL INFORMATION:
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: PARANHOS-BACCALA, Glaucia
APPLICANT: MALLET, Francola
TITLE OF INVENTION: ENDOGRNEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH AN
TITLE OF INVENTION: AUTOIMMUNE DISEASE, LABELING METHOD AND REAGENT
FILE REFERENCE: 110048
CURRENT APPLICATION NUMBER: US/10/632,793
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
SPRIOR FILING DATE: 1999-01-21
SPRIOR FILING DATE: 1999-01-21
SPRIOR FILING DATE: 1000-01-31
SSO ID NOS: 33
SSO ID NO 25
SSO ID NO 25
SSO ID NO 25
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                                         AAGCAGTTAGAGCGGTSGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA
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Pred. No. 1.6e-213;
0; Mismatches 75;
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Best Local Similarity
Matches 787; Conserv
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US-10-632-793-25
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                                                                                                                 AGGGGAAGAATGCTGTTAGTATGTTAATCTAGAATCATTACTGAGAAGTTAAAGA
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                                                              Score 712.6; DB 17
Pred. No. 1.2e-210;
0; Mismatches 81;
SOFTWARE: Patentin version 3.1
                                                                Query Match
Best Local Similarity 89.4%;
Matches 782; Conservative
                           TYPE: DNA
ORGANISM: Homo sapiens
US-10-632-793-26
                   LENGTH: 2782
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                                                           APPLICANT: Contad, Bernard
APPLICANT: Contad, Bernard
TITLE OF INVENTION: Multiple Sclerosis-Related Superantigen
TITLE OF INVENTION: Multiple Sclerosis-Related Superantigen
FILE REFERENCE: 23135-507
CURRENT FILING DATE: 2002-04-26
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                     53.5%; Score 711; DB 17;
89.3%; Pred. No. 3.9e-210;
tive 0; Mismatches 82;
                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Human endogenous retrovirus
; Sequence 1, Application US/10133036
; Publication No. US20040054133A1
; GENERAL INFORMATION:
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Best Local Similarity 89.37
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US-10-133-036-1
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  D IN BT474, SIGNAL = 5.9
IN FETAL LIVER, SIGNAL = 0 IN ADULT LIVER, SIGNAL = 0 IN BRAIN, SIGNAL = 6.2
D IN BONE MARROW, SIGNAL = 6.2
D IN LUNG, SIGNAL = 3.9
IN HELA, SIGNAL = 7.2
                                                                                                                                                                                 Score 704.8; DB 9;
Pred. No. 2.7e-208;
0; Mismatches 79;
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CTHER INFORMATION: EXPRESSED IN OTHER INFORMATION: EXPRESSED IN OTHER INFORMATION: EXPRESSED IN OTHER INFORMATION: EXPRESSED IN OTHER INFORMATION: EXPRESSED IN OTHER INFORMATION: EXPRESSED IN OTHER INFORMATION: EXPRESSED IN US-09-864-761-444
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APPLICANT: Rank, Sharron G.

APPLICANT: Rank, Sharron G.

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APPLICANT: Rank, Sharron G.

APPLICANT: Rank, Sharron G.

APPLICANT: Rank, Sharron G.

TITLE OF INVENTION: HUMAN GRNOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GRNOME-DERIVED SINGLE EXON NUCLEIC ACID FROMES TO CONTRIBUTE AND THE STATE AND THE STATE ACID GRNOMER: US 60/180, 312

REIGN RAPPLICATION WANRER: US 60/180, 312

REIGN FILING DATE: 2000-05-33

REIGN FILING DATE: 2000-05-33

REIGN FILING DATE: 2000-05-33

REIGN FILING DATE: 2000-05-34

REIGN FILING DATE: 2000-05-35

REIGN FILING DATE: 2000-05-35

REIGN FILING DATE: 2001-01-30/1801/0666

REIGN FILING DATE: 2001-01-30/1801/0666

REIGN FILING DATE: 2001-01-30/1801/0666

REIGN FILING DATE: 2001-01-30/1801/0666

REIGN FILING DATE: 2001-01-30/1801/0666

REIGN FILING DATE: 2001-01-30/1801/0666

REIGN FILING DATE: 2001-01-30/1801/0666

REIGN FILING DATE: 2001-01-30/1801/0666

REIGN FILING DATE: 2001-01-30/1801/0667

REIGN APPLICATION WANGER: PCT/USO1/0667

REIGN APPLICATION WANGER: PCT/USO1/0666

REIGN APPLICATION WANGER: PCT/USO1/0666

REIGN APPLICATION WANGER: PCT/USO1/0666

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REIGN APPLICATION WANGER: PCT/USO1/0667

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OTHER INFORMATION: MAP TO AC002346.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = OTHER INFORMATION: EXPRESSED IN HBART, SIGNAL = 5.4
                                                                                                                                                                                 2730 CATGCTATTTCACTCTTTAATCTTGCAACTGCA 2764
                                                                                                                                                   CACTCTATTTCACTCTATTAAATCATGCAACTGCA 875
                                                                                                                                                                                                                                                                                      Sequence 4444, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-09-864-761-4444
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Sequence 385, Application US/09854867

Sequence 385, Application US/09854867

Publication No. US20030224356A1

GENERAL INFORMATION.

GENERAL INFORMATION.

TOTAL OWN. RNOLL H

APPLICANT: OOAN, ENTER K

TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING.

TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING.

FILE REFERENCE: 30307

CURRENT FILING DATE: 2003-05-08

NUMBER OF SEQ ID NOS: 613

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 385

LENGTH: 780
                100298 TITCCIAGGCCGACIAAGAAICCCAAAGCCIAGCIGGGAAGGIGACCACAICCCCCITIA 100239
                                                                                                                                   100238 AACACTGGGCTTGCAACTTAGCTCACACCGACCAATCAGGTAGTAAAGAGAGCTCACTA 100179
                                                                                                                                                                                                                               100178 AAATGCTAATTAGACAAAAACAGGAGGTAAAAAATAGCCAATCATCTATCGCCTGAGAG 100119
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Best Local Similarity 90.0%; Pred. No. 1.3e-187;
Matches 711; Conservative 0; Mismatches 60; I
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VS-09-854-867-385
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85.4%; Pred. No. 4.1e-188;
tive 0; Mismatches 88; Indels
                                                                      Sequence 730, Application US/10087192

Publication No. US20020182586A1

GENERAL INFORMATION:
APPLICANT: Moris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
FILE REFERENCE: 522452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT PILING DATE: 2002-03-01

PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02

SROFTWARE: FESTEEQ for Windows Version 4.0

SEQ ID NO 730-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(161334)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 85.4
Matches 781; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                           45.3%; Score 601.4; DB 18; Length 157090; 87.0%; Pred. No. 5e-175; 2.1ve 0; Mismatches 84; Indels 19; G
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Publication No. US20040156832A1
GENERAL INFORMATION:
APPLICANT: JOJIN, Chris
TITLE OF INVENTION: Immunoglobulin Compositions and Methods
FILE REPRENCE: 1331.1001U
CURRENT APPLICATION NUMBER: US/10/672,764A
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
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Best Local Similarity 87.0
Matches 689; Conservative
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US-10-672-764A-34/c
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ORGANISM:
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; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17907, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL,
ATTLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
FULLS REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 17907
SEQ ID NO 17907
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   ------TITCACTCTATTAAATCTTGCAACTGCACTCTTCTGGTCGGGTTTGTTACG
                                                                                1020 TACCCATTGCCACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGC
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46.5%; Score 618; DB 19; Length 108773;

Best Local Similarity 88.8%; Pred. No. 2.8e-180;

Matches 695; Conservative 1; Mismatches 69; Indels 18;
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NAME/KEY: misc_feature
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US-10-741-600-17907
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                                                                            547 ACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGG
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                        DB 13; Length 180557;
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                                                  IndelB
                        Score 579.8; DB 13
Pred. No. 2.9e-168;
0; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Squence 9, Application US/10003806; Publication No. US20020119929A1; GENERAL INFORMATION: APPLICANT: Bishop, Colin B.; APPLICANT: Agoulnik, Alexander I.; APPLICANT: ADL, Qichao; TITLE OF INVENTION: CAN I AND ITS ROI; FILE REFERENCE: P02066US1/10024824
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                         43.6%;
86.0%;
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                                      Similarity 86.0
13; Conservative
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US-10-003-806-9/c
                                       Best Local Sim:
Matches 683;
US-10-003-806-6
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| Publication No. US20020119929A1
| GENERAL INFORMATION |
| APPLICANT: Bishop, Colin E. |
| APPLICANT: Agoulnik, Alexander I. |
| APPLICANT: Agoulnik, Alexander I. |
| APPLICANT: Agoulnik, Alexander I. |
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| APPLICANT: Agoulnik, Alexander I. |
| APPLICANT: Agoulnik, Alexander I. |
| FILE REFERENCE: P02066US1/10024824 |
| CURRENT FILING DATE: 2000-11-03 |
| PRIOR APPLICATION NUMBER: 60/245, 872 |
| PRIOR FILING DATE: 2000-11-03 |
| NUMBER OF SEQ ID NOS: 14 |
| SOFTWARE: Patentin version 3.1 |
| SEQ ID NO 6 |
| LENGTH: 180557 |
| TYPE: DNA |
| ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                         VASCULAR DISEASE
                                                                                                                                                                                                                                                                                                                                                                         Score 570.2; DB 15; Length.
Pred. No. 2.7e-165;
0; Mismatches 71; Indels
                                                                                                                                                        assigned
                                                                                                                                                        yet
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                                                                       TITLE OF INVESTIGATION: DIAGNOSIS AND TREATMENT OF FILE REFERENCE: MMI-008
TURENT APPLICATION NUMBER: US/10/017,117
CURRENT APPLICATION NUMBER: US/20030124535A1
PRIOR APPLICATION NUMBER: No. US20030124535A1
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                  g
                             ; Sequence 1, Application US/10017117; Publication No. US20030124535A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(161671)
; OTHER INFORMATION: n = a,t,c or
US-10-017-117-1
                                                                                                                                                                                                                                                                                                                                                                           Query Match

Best Local Similarity 88.5%;
Matches 655; Conservative
                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
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                                                                                                                                                                                        Score 579.8; DB 13;
Pred. No. 2.9e-168;
0; Mismatches 90;
; CURRENT APPLICATION NUMBER: US/10/003,806
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,872
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 9
; LENGTH: 180557
; TYPE: DNA
; OFGANISM: Human
US-10-003-806-9
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Best Local Similarity 86.0%;
Matches 683; Conservative
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APPLICANT: PERRON, HERVE
APPLICANT: BESEME, FREDERIC
APPLICANT: BESEME, FREDERIC
APPLICANT: PREDERIC
APPLICANT: PREDERIC
APPLICANT: PARANHOS-BACCALA, GLAUCIA
APPLICANT: AOLIVET-REYNAUD, COLETTE
APPLICANT: JOLIVET-REYNAUD, COLETTE
APPLICANT: ANDRAND, BERNARD
APPLICANT: TUKE, PHILIP
APPLICANT: TUKE, PHILIP
TITLE OF INVENTION: ASSOCIATED WITH MULITPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
TITLE OF INVENTION: THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                               1258 TGGCCCACTGCCATTTTGGTAGCGGCCCACCATCTTGGGAGCTGTGGGAGCAAGGAT 1317
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                                    55137 GCCCAGGTTCTTCCTAATCGAGCTGAACACTAGTCACTGGG-TCCACAGTTCTCTTCCGT
                                                                                                                                                          1138 GACCCACGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCCAAGATTCCATTCCTTG
               GGTACCCATTGCCACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGT
                                                                                     GCCTGGGTTTGTCCTAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTCTTCCAT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847
FILING DATE: 26-NOV-1997
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P.O. BOX 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 102, Application US/08979847; Publication No. US20030039664A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEPAX: 703-836-787
INFORMATION FOR SEQ ID NO: 102: SEQUENCE CHARACTERISTICS: LENGTH: 635 base pairs TYPE: nucleic acid STRANDENESS: single
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ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
RECISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WP!
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & B
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MEDIUM TYPE: Floppy
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STRANDEDNESS:
TOPOLOGY: line
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US-08-979-847-102
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APPLICANT: Wetzel, Jon C.
APPLICANT: Wetzel, Jon C.
APPLICANT: Geneff, Wo C.
TYLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
TITLE OF INVENTION: Winder: US/10/240, 425
CURRENT APPLICATION NUMBER: US/10/240, 425
CURRENT FILING DATE: 2002-09-30
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1102
LENGTH: 134292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.9%; Pred. No. 1.3e-157;
Matches 680; Conservative 0; Mismatches 89; Indels 23; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 AL031983
US-10-240-425-1102
                                                                                                                                                                                           Sequence 1102, Application US/10240425
Publication No. US20040033502A1
                                                                                                74827 cacceccarcirecaacre 74846
                                                               CACTGCCATTTTGGTAGCGG 1282
                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Williame, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                            RESULT 24
US-10-240-425-1102
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Pred. No. 1e-158;
0; Mismatches 47; Indels
                                                                                                                                             Version #1.30
                                                                                                                                                       CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/10/114,104
FILING DATE: 03-Apr-2002
CLASSIFICATION: «UNKnown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION ON BER: 08/979, 847

REGISTRATION UNBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPXX: 703-836-6400
TELEPXX: 703-836-6400
TELEPXX: 703-836-2787
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 635 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 102
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Local Similarity 92.4%;
les 572; Conservative
                                                               COMPUTER READABLE FORM:
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
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                                                                                          Gaps
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                                                   Length 635;
                                                                                          Indels
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                                                     Score 545; DB 8;
Pred. No. 1e-158;
                                                   41.0%; Score 545; DE ilarity 92.4%; Pred. No. 1e-1 Conservative 0; Mismatches
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CORRESPONDENCE ADDRESSS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 102, Application US/10114104
Publication No. US20030198647A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                875
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BESEME, FREDERIC
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TUKE, PHILIP
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                                                                       Best Local Similarity
Matches 572; Conserv
MOLECULE TYPE:
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US-10-114-104-102
  , MOLECULE TYP:
US-08-979-847-102
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                                                                                                                                                                                                                                                                                                   106 GGGATTCTCCAAAGTGTTTGTCTCTTCCAGAATCAAAACTGTAAAACTACAAATTGTTCT 165
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                                                                                                                                                                                208 CCCCTTCTTAGGACCTCTAGCAGCTATAATATTTTTACTCCTCTTTGGACCCTGTATCTT
       ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040048253A1 LG:429446.1:2000FEB18
US-10-220-120-15
                                                                                                                                                                                                                                                                       268 CAACTICCTTGATTAAGTITGTCTTCCAGAATTGAAGCTGTAAAAGCTACAAATAGTTCT
                                                                                                                                      Gaps
                                                                                                                                      14;
                                                                                           DB 17; Length 849;
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; Sequence 6792, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
                                                                                           Score 536.2; DB 17;
Pred. No. 6.5e-156;
0; Mismatches 135;
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                                                                                           Query Match
Best Local Similarity 81.4%;
Matches 650; Conservative
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60/184,776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HODGSON, David M.
APPLICANT: HODGSON, Stephen E.
APPLICANT: LINCOLN, Stephen E.
APPLICANT: LINCOLN, Stephen E.
APPLICANT: LINCOLN, Stephen E.
APPLICANT: JACKSON, Stuart
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/10/220,120
CURRENT APPLICATION NUMBER: 60/184,777; 60/184,797; 60/184,698; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/184,777; 60/18
           Sequence 15, Application US/10220120 Publication No. US20040048253A1 GENERAL INFORMATION:
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KOSEBRRKY, Ann M.
ROSEBRRKY, Ann M.
RUSSO, Frank D.
STOCKDREHER, Theresa K.
DAFFO, Abbal
WRIGHT, Rachel J.
YAP, Pierre E.
YU, Jimmy Y.
BRADLEY, Diana L.
BRADLEY, Diana L.
BRADLEY, Mensheng
COHEN, Mensheng
                                                                                                            ||||||||| ||||||| || ATTAAATCTTGCAACTGAA 619
                                                                                                                                                                                                                                                                                                        APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: PANZER, Scott R.
APPLICANT: SPIRO, Peter A.
APPLICANT: SHAH, Purvi
APPLICANT: CHALUP, Michael S.
APPLICANT: CHALUP, Michael S.
APPLICANT: CHANG, Simon C.
APPLICANT: CHEN, Alice
APPLICANT: OF SA, Steven A.
APPLICANT: DAM, TAM C.
APPLICANT: DAM, TAM C.
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APPLICANT: DAM, TAM C.
APPLICANT: CHARGES, VINCENT
                                                                                  ATTAAATCATGCAACTGCA 875
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GREENAWALT, Lila B.
HILLMAN, Jennifer L.
JONES, Anissa L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 15
LENGTH: 849
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT:
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197
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or insertion/deletion polymorphism (see Tables 1
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                                                                                                                                                                                                           38.7%; Score 513.8; DB 19; Length 83.0%; Pred. No. 7.2e-148; ive 3; Mismatches 108; Indels
  FILE REFERENCE: CL001449
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17727
LENGTH: 80032
                                                                                                                                                     ; LOCATION: (1)...(80032)
; OTHER INFORMATION: n = A,T,C or G,
US-10-741-600-17727
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Matches 659; Conservative
                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                           NAME/KEY: misc_feature
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                                                                                                                                            FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(366710)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
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Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719, 993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARES FASESEQ for Windows Version 4.0
SEQ ID NO 6792
LENGTH: 366710
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39.9%; Score 530.6; DB 18;
Best Local Similarity 91.0%; Pred. No. 9.4e-153;
Matches 563; Conservative 0; Mismatches 56;
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                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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US-10-741-600-17727/c
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170582 CATCGGCCATCCTCCCCAACAGACTTTGGGTTTTCCTGTTGAGAGGGGGTACTCAGAGAC 170523
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1198 GTATCTGTGAGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTTGGGAAG 1257
                                                                                                                                                                                                                   | Sequence | Application US/09731231A | Sequence | Application US/09731231A | Sequence | Application US/09731231A | Sequence | Application US/002008218941 | GENERAL INFORMATION: GENERAL INFORMATION: TSOLATED HUMAN KINASE PROTEINS, NUCLEIC | TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND | TITLE OF INVENTION: THEREOF | TITLE OF INVENTION: THEREOF | FILE REPERENCE: CLOOLOR | CURRENT APPLICATION NUMBER: US/09/731,231A | CURRENT APPLICATION NUMBER: US/09/731,231A | NUMBER OF SEQ ID NOS: GOTWARR: FRANCE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE | CONTINUE 
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Pred. No. 7.3e-144;
0; Mismatches 62;
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NAME/KEY: misc feature
LOCATION: (1)...(326014)
COTHER INFORMATION: n = A,T,C or US-09-731-231A-3
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Best Local Similarity 88.7%;
Matches 557; Conservative (
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                                                                                        TGGCC 1262
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ORGANISM: Human
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38.5%; Score 512; DB 17; Length 17758;
Best Local Similarity 84.7%; Pred. No. 1.2e-147;
Matches 614; Conservative 0; Mismatches 93; Indels 18;
                                                                                                         Sequence 2833, Application US/10264237
; Sequence 2833, Application No. US20040009491A1
; GRERRAL INFORMATION:
    APPLICANT: BITS et al.
    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TILE REPERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR PAPLICATION NUMBER: DC 10-04
; PRIOR PAPLICATION NUMBER: US 60/205,515
; PRIOR APPLICATION NUMBER: US 60/205,515
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIN Ver. 3.1
; SEQ ID NO 2833
                 31061 ACCCGCCAGTAACA 31048
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-10-264-237-2833
                                                                               RESULT 30
US-10-264-237-2833/c
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                  170523
                                                                                                                                       Sequence 3, Application US/10751985
Publication No. US20040126861A1
GREERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILLE REPERENCE: CLOO1007CON
CURRENT APPLICATION NUMBER: US/10/751,985
CURRENT FILING DATE: 2004-01-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FRANKE FRANKE OF SEC OF WINDOWS VERBION 4.0
SEQ ID NO 3
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Pred. No. 7.3e-144;
0; Mismatches 62;
                                                                  170222 TTTCACTCTATTAAATCTTGCAACAGCA 170195
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Best Local Similarity 88.7%;
Matches 557; Conservative
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NAME/KEY: misc\_feature LOCATION: (1)...(283351) LOCATION: (1)...(283351) MS-10-719-993-7065 Sequence 7065, Application US/10719993

Bublication No. US2004026849A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPRENCE: CLO01496
FILE REPRENCE: CL001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7065
LENGTH: 283351 175044 175220 175340 174984 642 2, 175105 CTAAGAATCCCTAAGCCTAGCTGAGGAGGTGACCGCATCCACCTTTAAACACGGGGCTTG GGAGGTAAAGCAATAGCCAATCATTGCCTGAGAGCACAGGGGAAGGACAAGGATT CAACTTAGCTCACACCCGACCAATCAGAGGCTCACTAAAATGCTAATCAGGCAAAAACA 763 GGGATATAAACTCAGGCATTCAAGCCAGCAACCCCCTTTGGGTCCCCTCCCATT 283 GTTTGTCTTCCAGAATTGAAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCA 343 GATGCAGTCCATGACTAAAATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGCTC 403 TGATGTTAATGACATTGAAGTCACCCTCCCGAGGAAATCTCAACTGCACAACCCCTACT 463 ACACTCCAATTCAGTAGGAAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACT CTAAGAATCCCNAAGCCTANCTGGGAAGGTGACCGCATCCATCTTAAACATGGGGCTTG Gaps Query Match
36.0%; Score 478.6; DB 18; Length 283351;
Best Local Similarity 90.1%; Pred. No. 1.3e-136;
Matches 534; Conservative 1; Mismatches 52; Indels 6; G

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36.0%;
90.1%;
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Best Local Similarity 90.1
Matches 534; Conservative
                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
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1 LOCATION: (1)...(283331)

2 OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables US-10-741-600-17995
                                                                                                           APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOUG1499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 17995
LENGTH: 283351
TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 1.3e-136;
1; Mismatches 52; Indels
                                                                           Sequence 17995, Application US/10741600 Publication No. US20050026169A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              Query Match 36.0%;
Best Local Similarity 90.1%;
Matches 534; Conservative
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RESULT 35

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; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism
US-10-719-993-6815
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Pred. No. 3.8e-136;
1; Mismatches 52; Indels 6; Ga
                                                                                           ASSOCIATED WITH METHODS OF DETECTION AND
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; Sequence 6815, Application US/10719993
; Bublication No. US20040265849A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE OF INVENTION: ALZHEIMER'S DISEASE, MET
; FILE REPRENENCE: CLO01496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FEBSELSEQ for Windows Version 4.0
; SEQ ID NO 6815
LENGTH: 1980090
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US-10-741-600-17676
US-10-741-600-17676, Application US/10741600
Sequence 17676, Application No. US20050026169A1
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
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LENGTH: 2052
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                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1980090)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SSCTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 17676
LENGTH: 1980090
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Publication No. US20040053245A1

Publication No. US20040053245A1

GENERAL INFORMATION:

APPLICANT: Hyeeq, Inc.

APPLICANT: Tang, Y, Tom et al

TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides

THER REPERENCE: 21272-030

CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT FILING DATE: 2002-11-18
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                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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| Sequence 28, Application US/10632793 |
| Sequence 28, Application No. US20040048298A1 |
| Sequence 28, Application No. US2004004829BA1 |
| Sequence 28, Application No. US2004004829BA1 |
| APPLICANT: PARANGS-BACCALA, Glaucia |
| APPLICANT: PARANGS-BACCALA, Glaucia |
| APPLICANT: PARANGS-BACCALA, Glaucia |
| TITLE OF INVENTION: ENDOGENEOUS NUCLEIC ACID FRAGMENT ASSOCIATED WITH P |
| TITLE OF INVENTION: AUTOINMUNE DISEASE, LABELING METHOD AND REAGENT |
| FILE REFERENCE: 110048 |
| CURRENT APPLICATION NUMBER: US/10/632,793
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                                                                                                                                                                                                                                                                                                                        DB 17; Length 2052;
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                                                                                                                                                                                                                                                                                                                  Score 468.8; DB 17;
Pred. No. 1.1e-134;
0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                 257 CCCTGIAICTICAACTICCTIGITAAGTITGTCT
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR PRICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 678
                                                                                                                                                                                                                                                                                                                     Ouery Match 35.3%;
Best Local Similarity 88.5%;
Matches 533; Conservative
                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
US-10-276-774-678
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PRIOR APPLICATION NUMBER: US 09/
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1
SEQ ID NO 148
                                                                                                                                     Query Match
Best Local Similarity 88.8%;
Matches 539; Conservative
                                                                                              ORGANISM: Homo Bapiens
US-09-997-722-148
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US-10-087-192-1666
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US-09-1977-22-148
US-09-9977-22-148
Sequence 148, Application US/09997722
Sequence 148, Application US/09997722
Sequence 148, Application US_0040072154A1
Sequence 148, Application No. US20040072154A1
TEREPERION:
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-12-22
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                                                                                                                                                                                                           Length 3372;
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                                                                                                                                                                                                           35.0%; Score 465; DB 17;
89.7%; Pred. No. 2.2e-133;
iive 0; Mismatches 57;
        CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US/09/869,927
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: PCT/FR00/00144
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 33
SOSTWARE: Patentin version 3.1
SEQ ID NO 28
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; ORGANISM: Homo sapiens
US-10-632-793-28
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; Bublication No. US20020182586A1
; GENERAL INFORMATION:
   APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: CANCER
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087, 192
; CURRENT APPLICATION NUMBER: US/09/747,377
; PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                    57;
                                                                                                                                                                                             DB 11;
                                                                                                                                                                                             Score 465; DB 11
Pred. No. 6e-133;
0; Mismatches 5
09/198,586
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279726 CATTGGCCAACTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGTGGGGACTGAGAGAC 279785
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                                                                                                                                                                                                                                               12; Gaps
                                                                                                                                                                                                             Query Match 34.6%; Score 460; DB 13; Length 285020; Best Local Similarity 88.6%; Pred. No. 8.5e-131; Matches 535; Conservative 0; Mismatches 57; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 21, 2005, 19:18:30 Job time : 750.518 secs
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SEQ TWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1666
LENGTH: 285020
                                                                                                                        | FEATURE:
| NAME/KEY: misc feature
| LOCATION: (1)...(285020)
| OTHER INFORMATION: n = A,T,C or G
                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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Perfect score:

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Database

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Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

18t strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMV8PORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CR605851 21-JUL-2004
full-length cDNA clone CS0DE012YJ24 of Placenta of Homo sapiens
(human).
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Li W. Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                     AG099717 P
BAI121669 P
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Pred. No. 1.2e-202;
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Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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OY 661 ACCANTCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC 720	AATCATCTATTGCCTGAGAGCACAGGGGGGACAATGGTCGGGATATAAACCCAAGTC	Oy 781 TTCAAGCCAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT 840	841 CACTCT 846	Db 2744 CATGCT 2749		z	ACCESSION CR622175 VERSION CR622175.1 G1:50502982 KRSHORDS HTC: CNSLT_CDNA.	MISM	REFERENCE 1 (bases 1 to 2500) AUTHORS 11, W.B., Gruber, C., Jessee, J. and Polayes, D. ATTHORS 11, W.B., Gruber, C., Jessee, J. and Polayes, D.	K AL	SS	TITLE Direct Submission JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr	COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) prime 1st strand cDNA was primed with a NotI-oligo dith Not I and cloned	end enriched, double-Burand cons was digesced with not a min constitution to the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a distriction of Taritrogen	<pre>Bource</pre>	NSPORT_6"	Query Match 52.8%; Score 702; DB 3; Length 2500; Best Local Similarity 90.6%; Pred. No. 3.2e-201; Matches 763; Conservative 0; Mismatches 67; Indels 12; Gaps 1;	OY 1 TCAAAATCGAAGGCTTTAGACTTGCTAACCGCCAAAAGGGGGAACCTGTTTATTTTT 60	61	

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

12 (bases 1 to 1071)

13 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

14 Mul-length cDNA libraries and normalization

15 Mul-length cDNA libraries and normalization

16 May 5, 2003 this sequence version replaced gi:30374869.

17 Contact: Genoscope

18 Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

2 rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

Email: seqref@genoscope.cne.fr. Web: www.genoscope.cne.fr

18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and Ecor V sites of the pCNVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                 X365066 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA LONE CSDI046YA18 3-PRIME, mRNA sequence.
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Corganism="Homo sapiens"

/mol_type="mkNa"

/db_xref="taxon:9606"

/clone="CSDD1046YA18"

/tlssue_type="PLACENTA_COT_25-NORMALIZED"

/clone="lb="Thang sapiens PLACENTA_COT_25-NORMALIZED"

/note="lst strand cDNA was primed with a NotI-oligo(dT)

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KEYWORDS
SOURCE
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- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Pred. No. 2.7e-200;
                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO44YK06"
/tissue_type="Placenta Cot 25"
/plasmid="pcMVSPORT_6"
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larity 90.6%;
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528

768 120 708 180 648 240 588

9

Gaps

ORIGIN	Query Match 51.1%; Score 678.6; DB 3; Length 2716; Best Local Similarity 90.5%; Pred. No. 4.3e-194; Matches 739; Conservative 0; Mismatches 66; Indels 12; Gaps 1;	OY 1 TCAAAATCGAAGGCTTTAGACTTGCTAACGGCGAAAGGGGGGAACCTGTTTATTTT 60	Oy 61 AGGGGAAGAATGCTGTTAGTATGTTAATCAATCTGGAATCATTACTGAGAAAGTTAAGA 120	OY 121 AATTTGAGATCGAATATAATGAGCGGAGCACCTTCAAAACACTGCACCCTGGGGCCT 180	Oy 181 CCTCAGCCAATGGATGCCCTGGACTCTCTTAGGACCTCTAGGAGCTATAATATT 240	OY 241 TITACTCCTCTTTGGACCCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTTTCCAGAAT 300	Oy 301 TGBAGCTGTAAAGCTACAAATAGTTCTTCAAATGGAACCCCAGATGCAGTCCATGACTAA 360	Qy         361 AATCTACCGTGGACCCCTGGACCGGCCTGCTAGACTATGTTAATGACATTGA 420	Oy 421 AGTCACCCCTCCCGAGGAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG 480 .	Qy         481 AAGCAGTTAGAGCAGTTAGTCAGCCAACCTCCCCAACAGTACTTTGGGTTTTTCCTGTTGAGA 540           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	541 2440	601	OY 661 ACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCC 720	Qy 721 AATCATCTATTGCCTGAGAGCACAGGAGAAGACAAGGATTGGGATATAAACTCAGGCA 780	Oy 781 TTCAAGCCAGCAACCCCCTTTGGGTCCCCTC 817 	LOCUS BX337769 998 bp mRNA linear EST 07-APR-2004 DEFINITION BX337769 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0D1051YM13 3-PRIME, mRNA sequence.	ACCESSION BX337769.2 GI:46272079 VERSION BX337769.2 GI:46272079 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens	
Db 527 CGAAGCTGTAAAACTACAAATGGAGCCCAAGATGCAGTCCAAGACTAA 480	Qy 361 AATCTACCGTGGACCCCTGGCTGCTAGACTATGCTCTGATGTTAATGACATTGA 420	Qy 421 AGTCACCCCTCCCGAGGAAATCTCAACTGCACAACCCCTACTACAATTCAGTAGG 480	Qy 481 AAGCAGTTAGAGCAGTTGTCGGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA 540	Qy 541 GGGTGGACTGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCT 600	OY 601 ANCTGGGAAGGTGACCGCATCCATTAAACATGGGGCTTGCAACTTAGCTCACCCG 660	OY 661 ACCAATCAGAGACTCACTAAAATGCTAATCAGGCAAAAACAGAGGTAAAGCAATAGCC 720 	Qy 721 AATCATCTATTGCCTGAGAGCACAGGACAAGGATATGGGATATAAACTCAGGCA 780 	OY 781 TTCAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT 840	RESULT 6 CR613169	_	ACCESSION CR613169.1 GI:50493976 KEYWORDS HTC; CNSLT_cDNA. SOURCE Homo appiens (human)			Faraday Avenue REFERENCE 2 (bases 1 to 2716) AUTHORS Genoscope. TITLE Direct Submission	JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) COMMENT 1st strand CDNA was primed with a NotI-oligo(dT) brimer. Five brime	FEATURES Location/Qualifiers  Source 1	/mol_type="mRNA" /db_xref="taxon:9606" /clone-type="1013120" /tissue_type="Placenta" /plasmid="pcMvSPORT_6"	

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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoP V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1058 bp mRNA linear EST 23-APR-2004
BX378303 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone CSODI018YH07 3-PRIME, mRNA sequence.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Li, Ubases 1 to 1058)
Li, W. B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Ompublished (2001)
On May 8, 2003 this sequence version replaced gi:30439129.
Contact: Genoscope
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                                                                                                       AGGGTGGACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCC
                       TANCTEGGAAGGTGACCGCATCCATCTTAAACATGGGGCTTGCAACTTAGCTCACACCC
                                                                                                                                                                 GACCAATCAGAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGC
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Pred. No. 6.2e-189;
1; Mismatches 92;
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/db_xref="taxon:9606"
/c1one="CS0DI018YH07"
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                                                                                                                                                                          Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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          Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="PLACENTA COT 25-NORWALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="1st strand cDNA was primed with a NotLo-ligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Ind I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                Catarrhini; Hominidae; Homo
                                                                                                                                 gi:30337641
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                              Mammalia, Butheria, Primates, Catarrhini, Homin
1 (bases 1 to 998)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Unpublished (2001)
On May 2, 2003 this sequence version replaced
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Pred. No. 2e-191;
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|db_xref="taxon:9606"
|clone="CS0DI051YM13"
               Chordata;
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Contact: Genoscope  Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage Genoscope - Centre National de 191657 EVRY cedex - FRANCE Email: segref@Genoscope.cns.fr, Web: www.genoscope.cns.fr  Ist strand cDNA was primed with a NotI-oligo(dT) primer: Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.  This sequence belongs to sequence cluster, see http://www.genoscope.cns.fr/cdna?s=CSODE012DE12NP1&c=4215.r. For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODE012DE12NP1&c=4215.r. For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODE012DE12NP1&c=4215.r.  FEATURES  1. 0103 //crganism="Homo sapiens" //mol_type="Hemo sapiens" //dolone="CSODE012V374" //clone="CS	Query Match         49.1%;         Score 652.2;         DB 5;         Length 1019;           Best Local Similarity         85.5%;         Pred. No. 3.3e-186;           Matches 725;         Conservative         19;         Mismatches         91;         Indels         13;         Gaps         2;           Qy         1         TCAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTATTTTT         60         835         TCAAAAATCGAAGAGCTTTAGACTTGCTAAACCGCTGAAAAGAGGGGGAACCTGTTATTTTT         776	Oy 61 AGGGAAGAATGCTGTTAGTTAATCAATCTGGAATCTTACTGAAAGTTAAAGA 120	1	Qy         361 AATCTACCGTGGACCCCTGGACCTGCTAGACTATGCTCTGATGTTAATGACATTGA         420           Bb         487 GATCTACCGCAGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAA         428           Qy         421 AGTCACCCCTCCGAGGAAATCTCAACTGCACACCCCTACTACATTCAGTAGG         480           427 AGCACCCTCCTGAGGAAATCTCAGCTGMACAACCCTATACTACGCAGG         368           Qy         481 AAGCAGTTAGAGCAGTTGTCAGCTGCAACCTCCCCCAACAGTTTCCTGTTGAGG         540           Qy         481 AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCCAACAGTTTTCCTGTTGAGG         369           Qy         481 AAGCAGTTAGAGCAGTTGTCAGCCCAACCTCCCCCACAGGCTTTTTCCTGTTGAGG         309           Qy         481 AAGCAGTTAGAGCAGTGACTGACCTCCCCCACAGGCTTTTTGAGGTTTTTCCTGTTGAGG         308           Qy         481 AAGCAGTTAGAGCAGCTGACTGACTGACTAAGATTCCCTAAGGTTTTCCTGTTGAGG         309           Qy         541 GGGGGACTGAGAAGGACTAGCTGGATTTCCTAAGGTTTCCCTAAGGTTTCCCTAAGGTTTTCCTTAAGGTTTTCTGTTTTAAACATGGGCTGACTAAGATCCCTAAGGCTTAAGCTTTTTAAACATGGGGCTTAAGGTTTTCCTTAAGGTTTTTTTT
	Qy         421 AGTCACCCCTCCCGAAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGG 480           Db         424 AGGCACCCCTCTGAGGAAATCTCAGTGCACACTCTACTACTACGCCCAATTCAGCAGG 365           Qy         481 AAGCAGTTAGAGCAGTTGTCACACCCCCCAACAGTACTTGCGTTTAGAGTTTAGAGTTTAGAGAGAG		Oy         661 ACCAATCAGAAGCTCACTAAAATGCTAATCAGGCAAAACAGGTAAAGAATGACATAACC         70           Db         194	SULT 9 439636/c CUS EUS FINITION BY CESSION BX WORDS FINITION BX WORDS FORGANISM HG CORGANISM HG MA THILE TITLE FUL TOUTUNAL UN MAMENT OF

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Genoecope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequencecope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
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BX357208 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI022XJ18 3-PRIME, mRNA sequence.
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1 (bases 1 to 758)

11, W.B., Gruber, C., Jessee, J. and Polayes, D.

11, W.B., Gruber, C., Jessee, J. and Polayes, D.

Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30376125.

Contact: Genoscope
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                                    TTACTCCTCTTTGGACCTGTATCTTCAACTTCCTTGTTAAGTTTGTCTCTTCCAGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGGTTTTCCTGTTGAGA
           AATTTGAGATCGAATATAATGTAGAGCAGAGGACCTTCAAAACACTGCACCCTGGGGCCT
                                                                                               CCTCAGCCAATGGATGCCCTGGACTCTCCCTTTAGGACCTCTAGCAGCTATAATATT
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                                         ACCAATCAGAGGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCC 720
                                                                  TICAAGCCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTT 840
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/note="Tis strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
AGCTGGGAAGGTGACCACATCCACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCTG 188
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82.5%; Pred. No. 2.2e-173;
tive 24; Mismatches 110; Indels
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Homo sapiens
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602852690F1 NIH_MGC_10 Homo sapiens CDNA Clone IMAGE:4993894 5',
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.5 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llh.gov
Plate: LiAM11015 row: d column: 23
High quality sequence stop: 762.
Location/Qualifiers
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89.2%; Pred. No. 2.3e-168;
iive 0; Mismatches 68;
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/cell line="MGG36"
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                                                                                                                                    /organism="Homo sapiens"
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/note=Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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      into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                      4215.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODIO22DE09NP1&c=4215.r.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                    Length 758;
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                                                                                                                                                                                                                                                                                                                                  45.8%; Score 608.2; DB 5; 88.1%; Pred. No. 7.2e-173; ive 9; Mismatches 69;
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                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 73 Row: k Column: 22 This clone has the following problem: retained intron. Location/Qualifiers
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.rGmail.nih.gov
Tissue procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shirs
Toshiyuki and Piero Carninci (NIKEN)
CDNA Library Arrayd Preparation: Miklos Piero (Systems Biology
CDNA Library Arrayd by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadanassystemsbiology.org
Anup Madan, Jossica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1064 TGGCTAAGAATCCCTAAGCCTAGGGAAATTGACCACGTCCACCTTTAAACACGGGGC
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/clone_lib="NIH_MGC_95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.5%; Score 592; DB 3; Local Similarity 81.1%; Pred. No. 1e-167; hes 755; Conservative 0; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab host="DH10B"
/note="Vector: pBluescript"
                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .4204
/organism="Homo Bapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5265109"
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Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Colline, F.S., Wagner, L., Schenmen, C.M., Schuler, G.D.,
Klausner, R.D., Colline, F.S., Wagner, L., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moorat, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morkernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanius, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC035153 4204 bp mRNA linear HTC 19-NOV-2003
Homo sapiens hypothetical protein FLJ22313, mRNA (cDNA clone
MAMOE:5565109), with apparent retained intron.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4204)
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Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
                                                                              CCCAATTCAGCAGGAAGCAGTTAGAGCGGTCGTC-GGCAACCTCCCCAAAAGCACTTAGG
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                                         TCCAATTCAGTAGGAAGCAGTTAGAGCAGTTGTCAGCCAACCTCCCCAACAGTACTTGGG
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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BC035153.1 GI:23272890
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Homo sapiens
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a Notl-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
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BX455153 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE013YI20 3-PRIME, mRNA sequence.
BX459153
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Catarrhini; Hominidae; Homo.
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                           GAACCCCAGATGCAGTCCATGACTAAAATCTACCGTGGACCCCTGGACCGGCCTGCTAGA
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31021096.
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Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Blotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
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Insert Length: 719 Std Error:
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Matches 657; Conservative 0
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/note="Wector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1002)
Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B., Mewes, H.W., Well, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
96 MVCCATSCACTGCCTGAGAGCACRGCAGGAGGAGACVATGMGCGGGAGRTAAASCCAAGTC 37
                                                                                                                                                                                                                                                                                                                                                                                                                               EST (Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., et al.)
Unpublished (2003)
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This clone (DKFZp70s1M064) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Enail S. wiemann@dkfz- heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germanny) within the CDNA sequencing consortium of the
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Pred. No. 4e-140;
0; Mismatches 72;
                                                            814
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                                                                               BCCGCCGGCCGGCTACGGCKCCCCCTKTGGTCCCC
                                                              781 TTCAAGCCAGCAACAGCAACCCCTTTGGGTCCC
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Acganism="Homo sapiens"
/mol_type="mRNA"
/db_xreff":taxon:9606"
/dcov stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                              BX953822.1 GI:43433374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.7%;
Best Local Similarity 87.6%;
Matches 641; Conservative 0
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BX953822/c
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KEYWORDS
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                                                                                                                                                                                                                /tissue_type="PlaCENTA"
/cissue_type="PlaCENTA"
/cione_lib="Homos saplens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
with a Not1-oligo(dT) primer. Five prime end enriched,
with a Not1 oligo(dT) primer of the pcmVsPORT 6 vector.
Library was not normalized."
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             normalized. Library was constructed by Life Technologies,
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
               was not normalized. Lize...

division of Invitrogen.

This sequence belongs to sequence cluster 4215.r

This sequence belongs to sequence cluster, see

This per more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CSODE013BE10NP1&c=4215.r.

http://www.genoscope.cns.fr/cdna?s=CSODE013BE10NP1&c=4215.r.

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                                                                                                                                                                                                                                                                                                                                                                             Length 900;
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Larity 77.5%; Pred. No. 2.5e-153;
Conservative 49; Mismatches 120; Indels
                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE013Y120"
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BM918330
AGENCOURT_6708649 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5747240
5', mRNA sequence.
BM918330.1 GI:19368709
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                                                                                                                                                                                                                                      5
                                                                                                                                                                                        679;
                                                                      /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                           Length
                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                        Score 480.8; DB 9;
Pred. No. 3.7e-134;
0; Mismatches 83;
                                                                                                                                                                                        Query Match
36.2%; Score 480.8;
Best Local Similarity 86.7%; Pred. No. 3.7e
Matches 552; Conservative 0; Mismatches
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-120G11.R"
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Totoki, Y., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submitssion

Submitted (02-AuG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

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Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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Pan troglodytes DNA, clone: PTB-120G11.R, genomic survey sequence.
AG113694
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                         TCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGTA-CCCAT
                                                                                                                                                                                                                                                                                                   TGCCACTCCCGATCAGGCTAAAGGCTTGCCA-TTGTTCCTGCATGGCTAAGTGCCTGGGT
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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Pan troglodytes
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Tokijyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Toyoda, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Tol. Subhiro-chou, Fsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone: PTB-147110.R, genomic survey sequence.
AG134524
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                 CTTGGTATCTGTGAGGCCAAGAACCCCAGGTCAGAGAANGTGAGGCTTGCCACCATTTGG
    CCATGACCCACGGCTTCTAATAGAGCTATAACACTCACGCCATGGCCCAAGATTCCATTC
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/clone_lib="PTB Chimpanzee Male BAC Library"
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/organism="Pan troglodytes"
/mol type="genomic DNA"
/db xref="taxon:9598"
/clone="PTB-147I10.R"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujiyama, A., Hattori, M., Toyoda, A.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                          1254 GAAGTGGCCCACTGCCATTTTGGTAGC 1280
                                                                                                                                                                                                                                     GAAGCAACCGCCACCATGTTGGGAGC 141
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R.Site 1 : SacI
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Location/Qualifiers
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                     /clone libe NNIH MGC 120"
/clone libe NNIH MGC 120"
/note="Organ: pooled pancreas and spleen; Vector:
pcMv-SpORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1:5 kb, insert size range 1-2:5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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                Email: capbs-remail.nil.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can information MGC clone distribution information can interp.//image.llnl.gov
http://image.llnl.gov
Plate: LLAMI2773 row: b column: 09
High quality sequence stop: 685.
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                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TMAGE:5747240"
/lab_host="DH108"
Strausberg, Ph.D.
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Totoki, Y., Watanabe, H. and Sakaki, Y.
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Pan troglodytes DNA, clone: PTB-030D19.F, genomic survey sequence.
AG049953
178 GCCAGCAACGGCAACCCCCTTTGGGT-CCCTCCCCTTGTATGGGAGCTCTGTTTTCACTC 236
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                                            TATTTCACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGGCTCAA
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                                                                  Taylor, T.D., Yada, T.
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/mol_type="genomic DNA"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             907 CTGAGCTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACAGACCCGCTGCTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 TGCTGCTCCTGATCGGGATAAAGGCTTGCCATTGTTCCTGCAAGGCTAAGTGCCTGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCACTCTATTAAATCATGCAACTGCACTC - TTCTGGTCCGTGTTTTTTATGGCTCAAG
                                                                                                                                                                                                                                           669 GAGAGCTCACTAAAATGCTAATCAGGCAAAAACAGGAGGTAAAGCAATAGCCAATCATCT
                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                               12;
                                          /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                  Length 669;
                                                                                                                                                                                                 Indels
                                                                                                                                                    Score 474; DB 9; I
Pred. No. 4.2e-132;
0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1267 GCCATTTTGGTAGCGGCCCACCACCATCTTG 1297
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCATTTTGGAAGCAGCCCGCCACCATGTTG
'db_xref="taxon:9598"
                     /clone="PTB-030D19.F"
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Pan troglodytes
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Direct Submission
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurum-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:91-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                GSS 03-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCTCACTAAAATGCTAATTAGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCCAT 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACTCTATTAAATCATGCAACTGCACTCTTCTGGTCCGTGTTTTTTATGGCTCAAGCTGA 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cacrerarecaarcriecaacrecacrerrenserrestringrandes de 304
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Pan troglodytes DNA, clone: PTB-097K23.F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell type="lymphoblast"
/clone lib="PTB Chimpanzee Male BAC Library"
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Pred. No. 9.4e-131;
0; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                          Pan troglodytes (chimpanzee)
Pan troglodytes
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larity 85.1%;
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R.Site 2
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CATTTT 681
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Matches 50
                                                                                                                                                                                                                              ACCESSION
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ORGANISM
                                                                                                                                                                                                    DEFINITION
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AUTHORS
                                                                                                                     RESULT 22
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (Oz.Aug. 2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (EIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:s1-45-503-911, Fax:81-445-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db xref="taxon:9598"
/clone="PTB-124K18.F"
/sex="malle"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.6%; Score 473; DB 9; Length 68 Best Local Similarity 88.8%; Pred. No. 8.6e-132; Matches 538; Conservative 0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
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BQ437925
AGENCOURT_7917208 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6161436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 943 whe batte: http://www.shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.
                                                                                                                                                               Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 41 Row: m Column: 10
This clone has the following problem: retained intron.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 468.2; DB 3;
Pred. No. 2.9e-130;
0; Mismatches 55;
                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
mol_type="mana"
db_xref="taxon:9606"
/clone="IMAGE:4724433"
/clone="IMAGE:4724433"
/clone_lib="NHIMGC"
/lab_host="DHIOF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pDNR-LIB"
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|AATCTTGCAACTACA 1131
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ilarity 90.1%;
Conservative
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Best Local Similarity
Matches 500; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1160)
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                               425 GCTCCCGATCGGGCTAAAGGCTTGCCATTGTTCCTGCACGGCTAAGTGCCTGGGTTCGTC
                                                                                                                                                                             CTAATAGAACTGAACACTGGTCACTGGGTTCCATGGTTCTTCCATGACCCACGGCTTC
                                                                                                                                                                                                   TAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGTATCTGTGAGGC
                                                                                                                                                                                                                                                                                      TAATAGAGCTATAAACACTCCACCGCATGGCCCAAGATTCCATTCCTTGGAATCCGTGAGGC
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                                                                                            1031 ACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC030968 1160 bp mRNA linear HTC 19-NO<sup>N</sup>
Homo sapiens CDNA clone IMAGE:4724433, with apparent retained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tisque Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                CAAGAACCCCAGGTCAGAGAACACGAGACT
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BC030968.1 GI:22658419
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Homo sapiens
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BC030968
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COMMENT
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Pan troglodytes (chimpanzee)
Pan troglodytes
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R.Site 1 : SacI
R.Site 2 : SacI.
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/mol type="mRNA"
/db Zref="Laxon:9606"
/db Zref="Laxon:9606"
/db Zref="Laxon:9606"
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/tissue type="melanotic melanoma"
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/clone lib="NIH MGC 72"
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Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 893)
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                                                                                                                                                                                                                   Email: cgapbe.remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13513 row: 1 column: 13
High quality sequence stop: 650.
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                                                                                                                                               MIN-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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5', mRNA sequence.
BQ437925
BQ437925.1 GI:21177001
                                                               Homo sapiens (human)
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Tokiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Tol. Subhiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tol:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end clone derived from the chimpanzee BAC library PTB This BAC end clone tracking errors.
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ATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCCTAATAGAACTGAACACTGGTCACTG 1116
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Pan troglodytes DNA, clone: PTB-064H14.R, genomic survey sequence.
AG072852
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                               Fujiyama,A., Hattbri,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabb,H. and Sakaki,Y.
BAC end sequences of Library PTB
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/clone_lib="PTB Chimpanzee Male BAC Library"
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Best Local Similarity 86.4%; Pred. No. 1.1e-126;
Matches 529; Conservative 0; Mismatches 74; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          AG121669
Pan troglodytes DNA, clone: PTB-130M15.F, genomic survey sequence. AG121669
AG121669.1 GI:16650834
GSS.
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                                                                                                                                                                                                                                                                           Gaps
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/organism="Pan troglodytes"

/mol_type="genomic DNA"

/mol_type="genomic DNA"

/db_xrefe="genomic DNA"

/db_xrefe="genomic DNA"

/clone="pTB-102B07.F"

/cell type="lymphoblast"

/cell type="lymphoblast"
                                                                                                                                                                                                                                         Length 712;
                                                                                                                                                                                                                                                                           76; Indels
                                                                                                                                                                                                                                         n 34.2%; Score 455; DB 9; I
Similarity 86.2%; Pred. No. 2.6e-126;
29; Conservative 0; Mismatches 76;
                                                             Location/Qualifiers
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Pan troglodytes
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Totoki, Y., Watanbe, H. and Sakaki, Y.
Totoki, Y., Watanbe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchitro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gac.riken.go.jp, URL:http://hgp.gac.riken.go.jp/,
Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                               1148
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                                                                                                                                                                                                                                                                                              CCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGTACCCATTG 1028
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Pan troglodytes DNA, clone: PTB-102B07.F, genomic survey sequence.
AG099717
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
GAGAGCTCACTAAAAAGCTAATTAGGCAAAAACAGGAGGTAAAAGAAATAGCCAATCATTT
                                                      AGCAACAGCAACCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTGACTCTAT
                                                                                                                              Accaacecrativeserrecerecerristareseacrerritrateacrerar
                                                                                                                                                                                                                                                     CCATCCCTCCGGATCCACCAGGGTGTCCACTGTGCTCCTGATCCAGCAAGGCGCCCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTAATAGAACTGAACACTGGTTCCATGGTTCTTCTTTCCATGACCCACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTAATAGAGCTATAACACTCACTGCATGGCCCAAGATTCCATTCCTTGGAATCCGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAAATCTTGCAACTGC-----GCTCTTCTGGTCTGCGTTTGTTACAGCTCAAGCT
                                                                                                                                                                                                                                GAGCTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGGTCACAGACCCGCTGCTGACTT
                                                                                                                                                                TTCACTCTATTAAATCATGCAACTGCACTCTTTTCTGGTCCGTGTTTTTTATGGCTCAAGCT
                                ATTGCCTGAGAGCACAGCGGAAGGACAAGGATTGGGATATAAACTCAGGCATTCAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes (chimpanzee)
Pan troglodytes
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GSS.
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AG099717
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637

ug-09-319-156b-12.rst

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/bx.refe="taxon:5759"
//bx.refe="taxon:5759"
//clone lib="Entamoeba histolytica Sheared DNA"
//clone lib="Entamoeba histolytica Sheared DNA"
//clone lib="Entamoeba histolytica Steel') Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Waking small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing. A Paracitcal Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                 Entamoeba histolytica
Entamoeba histolytica
Entamoeba histolytica
Entamoeba histolytica
Entamoeba histolytica
Entamoebidae; Entamoeba.

Ela (bases 1 to 921)

SS Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of Clone end sequences from Entamoeba histolytica
HM1: HMS sheared DNA library (2001)

Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1: IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 40
High quality sequence stop: 567.
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                                                                                                                                                                                                                               GSS 27-AUG-2001
186 TTATTGCCTGAGAGTACAGGGGAAGACACAATGATCGGGATATAAACTCATGCATTCGAG 127
                                                                                                                                                                                                                               ACTGAGAGACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCNAAGCCTANCTGG
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                                                                                              126 CCACCAATGGCTACCCTCTTTGGGTCCCCTCCCTTTGTTATGG
                                                                           787 CCAGCAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGG
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Pred. No. 2.4e-121;
0; Mismatches 84;
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                                                                                                                                                                                                                                                                               genomic, genomic survey sequence.
BH149565
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/strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                           BH149565.1 GI:15310303
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Best Local Similarity 83.8%;
Matches 550; Conservative 0
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BH149565/c
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokchama, Kanagawa 230-0045, Japan
(E-mall:chimpbes@gec.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                  Taylor, T.D., Yada, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pan troglodytes"
/mol type="genomic DNA"
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/clone="PTB-130M15.F"
/est="male"
/cell type="lymphoblast"
/cell type="lymphoblast"
/cell type="ptB-thmpanzee Male BAC Library"
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                                                                                Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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R.Site 1 : SacI
R.Site 2 : SacI.
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AG102951 683 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-106G16.F, genomic survey sequence.
AG102951
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGITIGICAGCCAACCICCCCAACAGIACITIGGGITITICCIGITIGAGAGGGIGGACIGAG 552
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Totoki, Y., Watunabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                    CGAGGAAATCTCAACTGCACAACCCCTACTACACTCCAATTCAGTAGGAAGCAGTTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 TGAGGAAATCTCAACTGCACAACCCCTACCATGCCCCATTCAGCAGGAAGCAGGTAGAG
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                                                                                                                         619;
                                  /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                           Length
                                                                                                                                                             Indels
                                                                                                                         Score 435.6; DB 9;
Pred. No. 2e-120;
0; Mismatches 76;
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db_xref="taxon:9598"
               clone="PTB-071A23.R"
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Pan troglodytes
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86.3%;
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                                                                                                                                                                   480;
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (102-MUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mall:chimpbes@gec.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIGCCIGGGITIGICCIAAIAGAACIGAACACIGGICACIGGGIICCAIGGIICTCTICC 1135
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                                                                                                                                                                                                                                                                                                                                     CCGCTGCTGACTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGC 1015
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                                                                                                                                                                                                                                                                                                243
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                                                             353
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Pan troglodytes DNA, clone: PTB-071A23.R, genomic survey sequence.
AG076758
 531 CAGGTAGTAAAAGAGGCTCACTAAAACGCTAATTAGGCAAAAAACAGGAGGTAAAAAA 472
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                  TATGGCTCAAGCTGAGCTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACAGAC
                                                                                                             GCATTCAAGCCAGCAACAGCAACCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGT
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BAC end sequences of Library PTB
Unpublished
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
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R.Site 1 : Sac1
R.Site 2 : Sac1.
Location/Qualifiers
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Euteleostomi;

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TGATCGGGATATAAACCCAGGCATTCGAGCCAGCAATGGCTACCCTTTGGGTCCCCTC 261
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                                                                                                                                                                                                                                                                                                                                                                     Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (lnfo@resgen.com). BAC end search page:
Research Genetics (lnfo@resgen.com). BAC end search bage:
Seq primer: SP6
                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 611)
Mano,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building.
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/clone_lib="RPC1-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 GAATTCCTAAACCTAGCTGAGAAGGTGACCGCATCCACCTTTAAACACGGGGCTTGCAAC
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                                                                                                                                                                                                                                   Unpublished (1997)
Other GSSB: RPCI11-165G20.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
Departmet for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
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genomic survey sequence.
AQ381711
                                     AQ381711.1 GI:4352734
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                                                                           Homo sapiens (human)
Homo sapiens
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           and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchitzo-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 11-7-22 Suchitzo-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sor.riken.go.jp), URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGTACCCA 1025
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                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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88.6%; Pred. No. 8.1e-120;
                                                                                                                                                                                                                                                                                            /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-106G16.F"
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                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                 : pKS145
                                                                                                                                                            Sequencing: -21M13
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Matches 514; Conservative
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R.Site 2
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LOCUS
DEFINITION
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Gaps

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757 201 817 875

Qy         790 GCAACAGCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTCACTCTATT         849           bb         610 ACAGCGGCTACCCTCGTTGGGTCCCCTTTGTATGGGTCTGTTTTCACTGTATT         551           Qy         850 TCACTCTATTAAATCATGCAACTGCACTCTTTGTATGGTCTAGTTTTTTATGGCTCAAGCTG         909           Db         550 AGGTCTTGCAAGTGCACACTCATTGGTCGTTTGTTATGGCTCAAGCTG         499           Qy         910 AGCTTTTGTTGCCACTCACTGCTGTTTGCACACGCTGGTGGTGGTG         499           AGCTTTGGATCCACCACCACTTTTGGAGCGCTGCTGGTGATTC         469           AGCTTTGGATCCACCACCACTTTTTGGAGCGCTGCTGATTCCTAGTCCAAACTCC         439           Qy         970 CATCCCTTTGGATCCACACACTGTTTTTTTTTTTTTTTT	030 CACTCCGGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGT 1089	Qy         1270 ATTTTGGTAGCGCCCACCACCACCACCACCACCACCACCACCACCACC		Email: mdddmmo@tlgr.org  Email: mdddmmo@tlgr.org  Clones are derived from the human BAC library RPCI-11. For BAC  Library avallablity, please contact Pieter de Jong  (pieter@delong.med.buffalo.edu). Clones may be purchased from  BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  Research Genetics (info@resgen.com). BAC end search page:  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html  Seg primer: SP6  Class: BAC ends.  Location/Qualifiers  FEATURES  Location/Qualifiers  // Organism="Homo sapiens"
	AG086046/C LOCUS AG086046 AG086046 AG086046 Total Innear GSS 03-NOV-2001 DEFINITION Pan troglodytes DNA, clone: PTB-084E11.R, genomic survey sequence. ACCESSION VERSION VERSION AG086046.1 GI:16637848 KEYWORDS GSS. SOURCE Pan troglodytes (chimpanzee) ORGANISM Pan troglodytes Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan. REFERENCE AUTHORS TOCOFI, Y., Watenabe, H. and Sakaki, Y. TOYOGA, H. and Sakaki, Y. TOTOFI, M. ARCHAPLES OF Library PTB TOTOFI, Y., PAC and seconences of Library PTB	AE RS	Sequencing: Miskev  LIBRARY Vector : pKS145  R.Site 1 : Saci R.Site 2 : Saci R.Site 2 : Saci Acation/Qualifiers Location/Qualifiers   1.736	Query Match         32.3%;         Score 429.4;         DB 9;         Length 736;           Best Local Similarity         81.8%;         Pred. No. 1.6e-118;         2;           Matches 522;         Conservative         0;         Mismatches 107;         Indels 9;         2;           Qy         670 AGAGCTCACTAAAATGCTAAT-TGGCGAAAAACAGGAGGAAAAACCATTCAACTA 671         2         3

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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoda, A., Taylor, T.D., Yada, T., Totoda, A., Toyoda, A., Taylor, T.D., Yada, T., Totoda, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totot, Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Totomical Research (RIKEN), Genomic Sciences Center (GSC);
Totomical Research (RIKEN), Genomic Sciences Center (GSC);
Totomical Research (RIKEN), Genomic Sciences Center (GSC);
Totomic Science (Form the Chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            969 CCATCCCTTTGGATCCAGCAGAGTGTCCACTGTGCTCCTGATCCAGCGAGGTACCCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 ACATCCTTCCGGATCCGGCAGGCGCCCGTTGTGTCTCCTGATCCAGCACGGCTCCCATTG
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                                               Taylor, T.D., Yada, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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ilarity 82.0%; Pred. No. 5.1e-117;
Conservative 0; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                          1. 697

| Organism="Pan troglodytes"

|mol_type="genomic DNA"

|db_xref="taxon:9598"

|clone="PTB-113D17.R"
                                                  Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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R.Site 1 : SacI
R.Site 2 : SacI.
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Matches 488; Conserv
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Pan troglodytes DNA, clone: PTB-113D17.R, genomic survey sequence.
AG108186
AG108186.1 GI:16728704
AG108166.1 GI:16728704
Pan troglodytes (chimpanzee)
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                                                                                         /cell_type="Lymphocytes"
/clond_lib="RoC1-11"
/noce="Vector: pBAC63.6; Site_1: EcoR1; Site_2: EcoR1;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                      291 ACTCTTCTGGTCCATGTTTGTTCCGGCTCAAGCTGAGCTTTTGCTCGCCGTCCACCACC
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                                                                                                                                                                                                                                                   ATCCCNAAGCCTANCT-GGGAAGGTGACCGCATCCATCTTTAAACATGGGGCTTGCAACT
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                                                                                                                                                                                                                     24;
                                                                                                                                                                                   Length 714;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                   32.2%; Score 427.6; DB 8;
llarity 83.0%; Pred. No. 5.5e-118;
Conservative 0; Mismatches 92;
          /mol_type="genomic DNA"
|db_xref="GDB:7524474"
|db_xref="taxon:9606"
|clone="RPCI-11-64L19"
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                                                                         /sex="Male"
                                                                                                                                                                                                      Similarity
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Qy         911 GCTTTTGTTCGCCATCCACCACTGCTGTTTGCCACCGTCACAGACCCGCTGCTGACTTCC         970           Db         304 GCTTTGCACCACCACCACTGCTGTTTGCC	1031 ACTCCCGATCAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTC 1090	Oy 1211 CAAGAACCCCAGGTCAGAANGTGAGGCTTGCCACTTTGGGAAGTGGCCCACTG 1267  Db 587 CAAGAAAGCTTGCCACCATCTTGGAAGTGGCCTGCCACCATTTGGAAGTGGTTCGCAC 646  Oy 1268 CCATTTG 1275  Db 647 CATCCTTG 654	RESULT 36 CB990962 LOCUS LOCUS CB990962 LOCUS CB990962 LOCUS DEFINITION AGENCOURT 13518713 NIH MGC_148 Homo sapiens cDNA clone IMAGE:30334786 5', mRNA sequence. ACCESSION CB990962.1 GI:30285482 KEYWORDS SOURCE Homo sapiens (human)	OKCANISM Homo baptens  DKCANISM Homo baptens  Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 (bases 1 to 797)  AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  COMMENT Email: cgapbs-r@mail.nih.gov  Tissue Procurement: Dr. Stefan Hansson  CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  and advice from Piero Carnino! (RIKEN)  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  DNA Sequencing by: Agencourt Bioscience Corporation	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:     http://image.llnl.gov     plate: NDAM355 row: j column: 11     High quality sequence stop: 661.     FEATURES	/ Mo.L Type="mknA" / db xrefe="taxon:9606" /clone="IMAGE:30334786" / fishe type="pre-eclamptic placenta" / lab hose="pre-ender
	_		JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)  COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.  PRIMERS Sequencing: -21M13	UIBRARY  Vector : pKS145  N.Site 1 : SacI  R.Site 2 : SacI.  R.Site 2 : SacI.  R.Site 2 : SacI.  Acoration/Qualifiers  1 . 675  Acoration="Pen troglodytes"  Acor	Query Match 31.9%; Score 423.8; DB 9; Length 675; Best Local Similarity 83.9%; Pred. No. 7.7e-117; Matches 510; Conservative 0; Mismatches 78; Indels 20; Gaps 2;  Qy 671 GAGCTCACTAAAATGCTAAAAAAAAAAAGGAAAAAAGGAATAGCCAATCATTT 730  bb 64 GAGCTCACTAAAAATGCTAATTAAAAAAAGCAAACAACAAGGAGGTAAAAAAAA	Qy         731 TGCCTGAGAGCACGGAAGGACTAGGATTAGGATTATAAACTCAGGCATTCAAGCCAG         790           Db         124 TGCCTGAGAGCACAGGAGGACGATGATCAGGATATAAACCCAGGCACTGGAGCCGG         183           Qy         791 CAACAGCAACCCCCTTTGGGTCCCCTCCCATTGTATGGAACTCTGTTTCACTCTATTT         850           Db         184 CAATGGCAACCCCTTTGGGTCCCTCCTTTGTATGGGAGCTCTGTTTTCACGCTATTT         243           Qy         851 CACTCTATTAAATCATGCACTCCACTCTTCTGGTCCGTGTTTTTTATGGCTCAAGCTGA         910           Db         244 CACTCTATTAAATCATGCACTCTTCTGGTCCATTTTTTTT

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1220 CAGGICAGAGAANGIGAGGCIIGCCACCAIIIGGGAAGIGGCCCCACIGCCAIITIGGIAG 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1040 CAGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCCTGGGTTTGTCCTAATAGAA 1099
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AGENCOURT 13642588 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30336351 5', mRNA sequence.
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Pred. No. 2.5e-116;
0; Mismatches 59;
                                                     sapiens"
ity sequence stop: 552.
Location/Qualifiers
                                   1. .803
/organism="Homo
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CB990802.1 GI:30285322
                                                                                                                                                                                                                                                                                                                                                                             31.8%;
ilarity 88.5%;
Conservative C
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sapiens
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CB990802
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Tissue Procurement: Dr. Stefan Hanson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Biosocience Corporation
Clone distribution: MGC clone distribution information can be
thtp://image.llnl.gov
Plate: NDAM362 row: a column: 12
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1 (bases 1 to 803)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                           91
 Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                             152 CACCGTCCACCACTGTTTGCCACCACGCGGGGGCTGCCGCTGACTCCCATCCCTCTG
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AGENCOURT 13623067 NIH MGC_148 Homo sapiens cDNA clone
IMAGE:30337259 5', mRNA sequence.
                                                                                       Length 797;
                                                                                                                           Indels
                                                                                          Score 422.2; DB 6;
Pred. No. 2.5e-116;
); Mismatches 59;
                                                                                                                            0; Mismatches
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CB992422.1 GI:30286942
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Homo sapiens
                                                                                                                            Conservative
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Matches 469;
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TITLE
JOURNAL
COMMENT
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211

271

919 151 979

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/tissue type="pre-eclamptic placenta"
/lab host="DHIOB TODA"
/lab host="DHIOB TODA"
/clonellab="MIH MGC_148"
/clonellab="MIH MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-Khol; Site_2: BamH; Library is oligo-dT primed_and
directionally cloned using primer
giretionally cloned using primer
5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average insert
size_2:3 kb and normalized to ROT 5. This is a primary
library enriched for full-lenght clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMI/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
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452 CAGGICAGAGAAIACGAGGCIIGCCACCAICTIGGAAGCGGCCIGCIACCAICIIGGAAG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I bases 1 to 831. Mag. No. 11H-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
Tissue Procurement: Dr. Stefan Hansson
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with he and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM348 row: p column: 01
High quality sequence stop: 611.
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AGENCOURT 13617032 NIH MGC 148 Homo sapiens cDNA clone
IMAGE:30332232 5', mRNA sequence.
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                                                                                                      Indels
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Pred. No. 2.5e-116;
0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3033232"
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KEYWORDS
SOURCE
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AUTHORS
TITLE
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COMMENT
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   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 826)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                       Email: cgapber@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with he
and advice from Piero Carninoi (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: NDAM359 row: k column: 16
High quality sequence stop: 585.
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larity 88.5%; Pred. No. 2.5e-116;
Conservative 0; Mismatches 59;
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                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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/tissue_type="ore-eclamptic placenta"
/lab_host="DH10B TonA"
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directionally cloned using primer
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size_2: 3 kb and normalized to RoT 5. This is a primary
library enriched for full-lenght clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Concact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information clone found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM366 row: p column: 12
High quality sequence stop: 708.
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(Dases 1 to 852)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
TATAACACTTACCACATGGCCCAAGATTCCATGGAATCCGTGAGGCCAAGAACTC
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AGENCOURT 13633532 NIH MGC 148 Homo sapiens CDNA clone IMAGE:30339155 5', mRNA sequence.
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Score 422.2; DB 6;
Pred. No. 2.5e-116;
0; Mismatches 59;
    31.8%;
88.5%;
  Query Match
Best Local Similarity 88.5
Matches 469; Conservative
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